

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 31, 2004, 07:16:51 ; Search time 6492 Seconds

(without alignments)
200.291 Million cell updates/sec

Title: US-09-987-190-2
Perfect score: 145
Sequence: 1 KXSLPHDYRSATEPYISQINEXYTX 30

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 segs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=x1h
-Q=/cgn2_1/USPRO.spool/US09987190/runat 24082004 161319 24730/app query.fasta_1.199
-DB=Genhmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0 -LOOFCU=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=ptco -NOR=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRR=US09987190.@CGN 1.1 3731 @runat 24082004 161319 24730 -NCPV=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGIOG
-DEV_TIMEOUT=120 -MAIN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Genhmbl.*
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38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	141	97.2	1859	8 AF031478	AF031478 Candida a
2	107	73.8	2332	8 CSMNSOD	Y11598 Candida sp.
3	103	71.0	621	6 AR257498	AR257498 Sequence
4	103	71.0	735	1 NAU02341	U02341 Nocardiella as
5	101	69.7	657	1 AF333434	AF333434 Mycobacte
6	101	69.7	900	6 AX708734	AX708734 Sequence
7	101	69.7	960	1 MAU11550	U11550 Mycobacteri
8	101	69.7	1741	1 AF180816	AF180816 Mycobacte
9	100	69.0	908	11 D13288	D13288 Mycobacteri
10	100	69.0	908	11 CNS06105	AL400539 T3 end of
11	100	69.0	2045	8 SCSDMMNG	X02156 Yeast gene
12	100	69.0	18715	8 YSCHL2825	U10400 Saccharomyc
13	100	69.0	24431	8 YSCH9780	U10555 Saccharomyc
14	99	68.3	1071	1 AF061031	AF061031 Mycobacte
15	99	68.3	1478	1 MFSODA	X70914 M.fortitum
16	98	67.6	649	1 MLEPSOD	X16453 Mycobacteri
17	98	67.6	344050	1 MLEPSOD	AL583917 Mycobacte
18	98	64.8	790	1 MLEPSOD	X2861 M.tuberculo
19	94	64.8	943	1 AF077406	AF077406 Mycobacte
20	94	64.8	1321	1 AF061030	AF061030 Mycobacte
21	94	64.8	1321	6 AX708732	AX708732 Sequence
22	94	64.8	14282	1 AE007188	AE007188 Mycobacte
23	94	64.8	244800	1 BX842584	BX842584 Mycobacte
24	94	64.8	278492	1 BX248347	BX248347 Mycobacte
25	91	62.8	567	1 PFSOD	X91650 P.firendre
26	91	62.8	567	1 PFSOD	Y09012 P.firendre
27	84	57.9	302529	1 AE016851	AE016851 Triopherym
28	82	56.6	239050	1 BX251411	BX251411 Triopherym
29	80	55.2	655	3 AB079877	AB079877 Marisupena
30	80	55.2	954	4 AB001693	AB001693 Equus cab
31	80	55.2	4439	1 GSP312188	AJ312188 Gordonia
32	79	54.5	812	6 E15569	E15569 CDNA encodi
33	79	54.5	812	6 AR222758	AR222758 Sequence
34	78	53.8	429	3 AY211085	AY211085 Farfante
35	78	53.8	349659	1 BX248360	BX248360 Coryneb
36	77	53.1	600	6 AX123311	AX123311 Sequence
37	77	53.1	606	6 BD165428	BD165428 Novel pol
38	77	53.1	606	4 RA8MSD	L28808 Oryctolagus
39	77	53.1	960	1 AB055218	AB055218 Coryneb
40	77	53.1	1143	6 AR338437	AR338437 Sequence
41	77	53.1	1143	6 AX136077	AX136077 Sequence
42	77	53.1	1143	6 BD011434	BD011434 DNA, amin
43	77	53.1	2207	1 AF236111	AF236111 Coryneb
44	77	53.1	302070	1 AP005223	AP005223 Coryneb
45	77	53.1	309400	6 AX127153	AX127153 Sequence

RESULT 1

ALIGNMENTS

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 LOCUS AF031478
 DEFINITION Candida albicans manganese-superoxide dismutase precursor (SOD2)
 gene, complete cds.
 AF031478
 ACCESSION AF031478.1 GI:2623884
 VERSION
 KEYWORDS
 ORGANISM Candida albicans
 SOURCE
 ORGANISM Candida albicans
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; mitosporic Saccharomycetales; Candida.
 REFERENCE
 1 (bases 1 to 1859)
 Rhee, G.R., Hwang, C.S., Brady, M.J., Kim, S.T., Kim, Y.R., Huh, W.K.,
 Baek, Y.U., Lee, B.H., Lee, J.S., and Kang, S.O.
 Manganese-containing superoxide dismutase and its gene from Candida
 albicans
 JOURNAL Blochim. Biophys. Acta 1426 (3), 409-419 (1999)
 MEDLINE 99177423
 PUBMED 10076057
 2 (bases 1 to 1859)
 Kang, S.O. and Rhee, G.
 Direct Submission
 TITLE Submitted (26-OCT-1997) Microbiology, Seoul National University,
 Shinlim-dong, Kwanak-gu, Seoul 151-742, Republic of Korea
 JOURNAL
 FEATURES
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 /db_xref="taxon:5476"
 848..1552
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 /db_xref="GI:2623885"
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 Score: 141.00 Matches: 27
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 Best Local Similarity: 96.43% Mismatches: 1
 Query Match: 97.24% Indels: 0
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 QY 1 LysTYrSerLeuProGluLeuAspTYrGluPheSerAlaThrGluProTYrIleSerGly 20
 Db 950 AAATVTAAATTTCACGAATTCGACATATTCCTCGCTACGACCACTATTCTGGT 1009
 QY 21 GlnIleAsnGluIle**TYrThr 28
 Db 1010 CAAATTAACGAATTCACCTACTACT 1033
 RESULT 2
 LOCUS CSMNSOD 2332 bp DNA linear PLN 11-MAY-2001
 DEFINITION Candida sp. HN95 MnSOD gene.

ACCESSION Y11598
 VERSION Y11598.1 GI:1877052
 KEYWORDS manganese superoxide dismutase; MnSOD gene.
 SOURCE Candida sp. HN95
 ORGANISM Candida sp. HN95
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; mitosporic Saccharomycetales; Candida.
 REFERENCE
 1
 Hong, Y.M., Nam, Y.S. and Choi, S.Y.
 Molecular Cloning and Characterization of Mn-Superoxide Dismutase
 Gene from Candida sp
 JOURNAL J. Microbiol. 35, 309-314 (1997)
 REFERENCE
 2 (bases 1 to 2332)
 Choi, S.
 Direct Submission
 TITLE Submitted (04-MAR-1997) S. Choi, HanNam University, Microbiology,
 133 Ojung-Dong, Taeduk-Xu, Taejeon, 300-791, SOUTH KOREA
 JOURNAL
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 1590..2180
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 Best Local Similarity: 71.43% Mismatches: 4
 Query Match: 73.79% Indels: 0
 DB: 8 Gaps: 0
 US-09-987-190-2 (1-30) x CSMNSOD (1-2332)
 QY 1 LysTYrSerLeuProGluLeuAspTYrGluPheSerAlaThrGluProTYrIleSerGly 20
 Db 1584 AAAGATGCTTACCAAGATTGGATTCGGACCTCGAGCCTCGAGCCTCACATTTCGGGA 1643
 QY 21 GlnIleAsnGluIle**TYrThr 28
 Db 1644 CAGATCAACGAATTCACCTACACC 1667
 RESULT 3
 LOCUS AR257498 621 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 23 from patent US 6486382.
 ACCESSION AR257498
 VERSION AR257498.1 GI:27307539
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

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REFERENCE
  Unclassified.
  1 (bases 1 to 621)
  Gordon-Kamm, W., Pierce, D.A., Bowen, B., Bidney, D., Ross, M.,
  Seelange, C., Miller, M.D., Sandahl, G. and Wang, L.
  Use of the green fluorescent protein as a screenable marker for
  plant transformation
  Patent: US 6486382-A 23 26-NOV-2002;
  Location/Qualifiers
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Best Local Similarity: 60.71% Mismatches: 2
Query Match: 71.03% Indels: 0
Gaps: 0

US-09-987-190-2 (1-30) x AR257498 (1-621)

QY 1 LysTyrSerLeuProGluIleuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
  ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 7 GAGTACACGCTCCCGGATCTGGATTACGACTACAGCCGCCCTGGAAACCCACATCTCCG 66
  QY 21 GlnIleAsnGluIle**TyrThr 28
  |||||:::
  67 CAGATCAACGAGCTGCACCATTC 90

RESUT 4
NAU02341
LOCUS NAU02341 735 bp DNA linear BCT 12-MAR-1996
DEFINITION Nocardia asteroides GUH2 superoxide dismutase gene, complete cds.
ACCESSION U02341
VERSION U02341.1 GI:484066
KEYWORDS
SOURCE
  Nocardia asteroides
  Nocardia asteroides
  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
  Corynebacterineae; Nocardiaceae; Nocardia.
  1 (bases 1 to 735)
  Alexander, D.J., Chapman, G.D. and Beaman, B.L.
  Isolation, sequencing and expression of the superoxide
  dismutase-encoding gene (sod) of Nocardia asteroides strain GUH-2
  Gene 164 (1), 143-147 (1995)
  96060954
  7590304
  2 (bases 1 to 735)
  Chapman, G.G.
  Direct Submission
  Submitted (01-OCT-1993) Gail D. Chapman, Medical Microbiology and
  Immunology, University of California at Davis, Medical Science
  Building 1A, Davis, CA 95616, USA
  Location/Qualifiers
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[illegible]

SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Mycobacterium avium subsp. paratuberculosis
Mycobacterium avium subsp. paratuberculosis
Bacteria; Actinobacteriia; Actinobacteriales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
avium complex (MBC).
1 (bases 1 to 1741)
Liu, X., Feng, Z., Harris, N.B., Cirillo, J.D., Bercovier, H. and
Barletta, R.G.
Identification of a secreted superoxide dismutase in Mycobacterium
avium ssp. paratuberculosis
FEMS Microbiol. Lett. 202 (2), 233-238 (2001)
21411748
11520620
2 (bases 1 to 1741)
Liu, X., Feng, Z., Cirillo, J. and Barletta, R.G.
Direct Submission
Submitted (25-AUG-1999) Veterinary and Biomedical Sciences,
University of Nebraska-Lincoln, Fair Street and East Campus Loop,
Lincoln, NE 68583-0905, USA
Location/Qualifiers
1. 1741
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Alignment Scores:
Pred. No.: 3,76e-08 Length: 1741
Score: 101.00 Matches: 17
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Best Local Similarity: 60.71% Mismatches: 2
Query Match: 69.66% Indels: 0
DB: 1 Gaps: 0
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QY 1 LysTyrSerLeuProGluLeuAspTyrGluPhseSerAlaThrGluProTyrIleSerGly 20
Db 266 GAATACACCTGCTGCCGACCTGGACTGAGACTATGACGCTTGGAACCGCACATCTGGGG 325
QY 21 GlnIleAsnGluIle***TyrThr 28
Db 326 CAGATCAACGAGATCCACACACACC 349
RESULT 9
D13288

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

D13288
Mycobacterium lepraemurium DNA for Mn superoxide dismutase,
complete cds.
D13288
D13288.1 GI:3228263
Mn superoxide dismutase.
Mycobacterium lepraemurium
Mycobacterium lepraemurium
Bacteria; Actinobacteriia; Actinobacteriales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 815)
Nakamura, M.
Unpublished
2 (bases 1 to 815)
Nakamura, M.
Direct Submission
Submitted (21-SEP-1992) Masahiko Nakamura, Osaka University,
Institute for Protein Research; 3-2 Yamadaoka, Suita, Osaka 565,
Japan (E-mail: masahiko@protein.osaka-u.ac.jp, Tel: 06-879-8628,
Fax: 06-879-8629)
Location/Qualifiers
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Pred. No.: 2,23e-08 Length: 815
Score: 100.00 Matches: 17
Percent Similarity: 89.29% Conservative: 8
Best Local Similarity: 60.71% Mismatches: 3
Query Match: 68.97% Indels: 0
DB: 1 Gaps: 0
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QY 1 LysTyrSerLeuProGluLeuAspTyrGluPhseSerAlaThrGluProTyrIleSerGly 20
Db 100 GAATACACCTGCTGCCGACCTGGACTGAGACTATGAAAGCTTGGAACCGCACATCTGGGG 159
QY 21 GlnIleAsnGluIle***TyrThr 28
Db 160 CAGATTACGAGATCCACACACACC 183
RESULT 10
CNS06105
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

CNS06105
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of Saccharomyces bayanus, sequence tagged site.
AL400539
AL400539.1 GI:12156708
STS.
Saccharomyces bayanus
Saccharomyces bayanus
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 908)
Souci, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,

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TITLE
JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS COMMENT
COMMENT
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1..908 /organism="Saccharomyces bayanus" /mol_type="genomic DNA" /strain="CLIB 533" /variety="uvatum" /db_xref="taxon:4931" /clone="ASOAA022C08" /clone_1lb="ASOAA" /note="end : T3" <4...>239 /note="similar to Saccharomyces cerevisiae ORF YHR009c [ similarity to S.pombe hypothetical protein ] I putative frameshift(s)" /evidence=not_experimental <673...>906 /note="similar to Saccharomyces cerevisiae ORF YHR008c [ SOD2 ; superoxide dismutase (Mn) precursor, mitochondrial ]" /evidence=not_experimental misc_feature /note="similar to Saccharomyces bayanus" Alignment Scores: Pred. No.: Length: 908 Score: 100.00 Matches: 18 Percent Similarity: 82.14% Conserved: 5 Best Local Similarity: 64.29% Mismatches: 5 Query Match: 68.97% Indels: 0 DB: 11 Gaps: 0 US-09-987-190-2 (1-30) x CNS06IOS (1-908) QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20 Db 751 AAAGTCACCTTGCCGAAGCGATTTGGGACTTTGGAACCATATTATTGGGC 810 QY 21 GlnIleAsnGluIle***TyrThr 28 Db 811 CAAATCAACGAATTCATTACACC 934

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SCSDOMNG	2045 bp	DNA	linear	PLN 04-DEC-1994
LOCUS				
DEFINITION	Yeast gene for mitochondrial manganese superoxide dismutase (MnSOD)			
ACCESSION	X02156			
VERSION	X02156.1	GI:4513		
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
MEDLINE				
PUBMED				
COMMENT				
FEATURES				
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ORIGIN				
Alignment Scores:				
6.97e-08				
Length:				
2045				

Score: 100.00 Matches: 18
 Percent Similarity: 82.14% Conservative: 5
 Best Local Similarity: 64.29% Mismatches: 5
 Query Match: 68.97% Indels: 0
 DB: 8 Gaps: 0

US-09-987-190-2 (1-30) x SCSDMMNG (1-2045)

QY 1 LysTyrSerLeuProGlnLeuAspTyrGluPheSerAlaThrGluProTyrIleSeryI 20
 Db 637 AAAGTCACTTGCAGACTGAAAGTGCAGTTCGGTGCACGTGAACCTTATATCTCCGCT 696
 QY 21 GlnIleasnGluIle***TyrThr 28
 Db 637 CAAATCAAGAAATTCATTACACC 720

RESULT 12
 LOCUS YSCHL2825 18715 bp DNA linear PLN 04-SEP-1997
 DEFINITION Saccharomyces cerevisiae chromosome VIII cosmid l2825.
 ACCESSION U10400 U00093
 VERSION U10400.1 GI:500701
 KEYWORDS
 SOURCE
 ORGANISM Saccharomyces cerevisiae (baker's yeast)
 Saccharomyces cerevisiae
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 1 (bases 1 to 18715)
 Johnston, M., Andrews, S., Brinkman, R., Cooper, J., Ding, H., Dover, J.,
 Du, Z., Favello, A., Fulton, L., Gattung, S., Geisel, C., Kirsten, V.,
 Kucaba, T., Hillier, L., Jier, M., Johnston, L., Keppler, D.,
 Langston, Y., Latreille, P., Louis, E., Macri, C., Mardis, E.,
 Mouser, L., Nhan, M., Rifken, L., Riley, L., St. Peter, H., Thornton, L.,
 Trevaaskis, E., Vaudin, M., Vaughan, K., Vignati, D., Wilcox, L.,
 Willis, A., Wilson, R., Wohldman, P. and Waterston, R.,
 Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
 VIII
 Science 265 (5181), 2077-2082 (1994)
 JOURNAL MEDLINE 94378003
 PUBMED 8091229
 2 (bases 1 to 18715)
 Du, Z.
 The sequence of S. cerevisiae cosmid l2825
 Unpublished (1994)
 3 (bases 1 to 18715)
 Waterston, R.
 Direct Submission
 Submitted (06-JUN-1994)
 4 (bases 1 to 18715)
 Jia, Y. and Cherry, J.M.
 Direct Submission
 Submitted (04-SEP-1997) Department of Genetics, Stanford
 University, Saccharomyces Genome Database, Stanford, CA 94305-5120,
 USA

COMMENT
 Curated by:
 Saccharomyces Genome Database
 URL: <http://genome-www.stanford.edu/>
 e-mail: yeast-curator@genome.stanford.edu
 Submitted by:
 Genome Sequencing Center
 Department of Genetics, Washington University,
 St. Louis, MO 63110, USA
 e-mail: mj@sequencer.wustl.edu

NEIGHBORING COSMID INFORMATION:
 This sequence includes nucleotides 1-17118 of lambda clone
 YSCH2825. It overlaps with the cosmid on the left (YSCH9780) by
 800 bp; with the cosmid on the right (YSCH8082) by 1001 bp.
 Location/Qualifiers

source 1..18715
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 /mol_type="genomic DNA"
 /strain="S288C (AB972)"
 /db_xref="taxon:4932"
 /map="VIII"
 /complement (128..829)
 /gene="SOD2"
 /complement (128..829)
 /gene="SOD2"
 /note="YHR008C"
 /codon_start=1
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 /protein_id="AAB68938.1"
 /db_xref="GI:500704"
 /translation="MFAYTAANLTKKGGSLSTTARTRTVTLPDLMKDFGALPEYI
 SGQINLELHYTHQTYVNGFNTAVDOFQELSDLAKEPSPNARKMLAIQONIKFGG
 GFTNHCFEMTLAPESQGGEPPTGALAKAIDFQGLDELKLTNTKLAGVCGGMA
 FIVKNI.SNGGKLADVQTYNDVTGPLVLVAIDAMHAYLYQNKKADYFKAIWV
 VMKKEASRRPAGKI"
 complement (1348..2904)
 /gene="YHR009C"
 /complement (1348..2904)
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 /codon_start=1
 /evidence=not experimental
 /product="Yhr009cp"
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 THHITTSIRVIGAGAGKAGLASAPPHQIVPLSPQHSLSDSDYDENMDYR
 LTVLSLEADPREVIEYVELSKAYNLVPPPKRGYTSNKNFIDSNLSLSSGS
 SIKSDASNSNEBSGDIVSSVSLHSLTNERMKSHTNSASDLSVSLQRLKTNTH
 NPLPADLWLRRLVNDVSSLGDDTQAQPKYFTFLISKMETGAVLLDGLKVV
 LKCDENDCVHSLXYLPSVVRNRNSRGAENPDIKGTIFENDEAKPIEINDIQOIVY
 SMGPWTSKILKDCPIGSLRAHSVTIKSEKTSPIYATLAKVNDREPPENYARD
 EYVCGEGDLTVNIPESDDVEVSEKCDLHYHVSLSPTLSKGHILRRQACPLV
 NVPTSSGPLIGETNVKDLTYASGHSCHGINNAPATGKLMAEIIILDGATSAEISSLP
 KLYFDATILS"
 3759..4730
 /gene="RP127"
 /join (3759..3789,4351..4730)
 /gene="RP127"
 /note="YHR010W"
 /codon_start=1
 /evidence=not experimental
 /product="Rp127p: Probable 60S ribosomal protein L27"
 /protein_id="AAB68944.1"
 /db_xref="GI:500709"
 /translation="MAKPLKAGKVAVVVRGKAGKVIVYKPHDSSKSHPHGHALVA
 GIERVPLKTVTKHGAKKVAKRTIKKPIKIVNINHLPIRYTLLDVEAFKSVSTETE
 QPSQREBAKVVAKFAEERHQKQWFSKLF"
 5018..6358
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 /note="Similar to Seryl-tRNA synthetase"
 /evidence=not experimental
 /codon_start=1
 /product="Yhr011wp"
 /protein_id="AAB68940.1"
 /db_xref="GI:500705"
 /translation="WIRRLSISNRSFPLKQPQDVKKIIMIPQYQTSIONRELIE
 AASITRSQQLGERYQNIKEIDKVLADIQKRSIAQIKKQTKTKTEYSALAKALKE
 QYNDQNSKSELDKRLKILFETCKSLPNTLDPTVLDLAPQIQMINKTKTEYSQAQAVD
 IMLKKMLDLQTSAVTGMSSVYLLNDGRLBOALVAVLAKKANENGSSCVPSITTK
 KELIDACGFNPRDNNEROIVALQDITNGLVATETPLAGLCANVLENSGSCSKL
 VGSRCVYRABAGARGDQTKGLRYHETVVELPCKSKPETSIAVLEIKQFQISVEE
 LGIPAKVNLMPENDGNPARKTDIEAMPBGKFGESASNCJDFQSRILNTKYRD
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 6719..7686
 /gene="VPS29"
 /join (6719..6766,6886..7686)

gene
 CDS

FEATURES

/gene="YB829"
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/evidence=not experimental
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sorting"
/protein_id="AAB68947.1"
/db_xref="GI:500712"
/translation="MTLLASDAHPDRAADLPVKKKKLLSPDKTSQVALLGNTKS
YDFLKTQVNOISNITIVRGFEFDHLPSTTKDASDSEWEETPMNSITRQALKIG
CCGGYIVPKNDDLSIALAROLDVILMGTHNVAATLBEKFPVNPBSCTGART
DMPDIVEDSDSDAVSDVETKRENSQSDDAKGSQGTGKQSGSTPKGKGEEN
ENSNVKEPQFKEDEVDMSDSDINSNSPFLDIQNTCTLIYLYLVNGHVKYDK
VYVEKE"
complement (7968. .8684)
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complement (7968. .8684)
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/codon_start=1
/product="Ard1p: subunit of the major N
alpha-acetyltransferase"
/protein_id="AAB68937.1"
/db_xref="GI:500702"
/translation="MPINRRATINDIICQONANLHNLPNYMMKYMYHILSPBAS
FVATTTLDGSDPDSDNDKIELTLDGTGRTIKDPTYLAGEKLGVYVYKMD
DPDQNEPPNGHTSLSVKRTYRMGAENMLRQALFALREHQAEEVSLAHQSNRA
ALHLYRDTLAEVLSISKSTYQDGEDAFAKKVAKLELQISNTHRLKNEKEED
DLBSLDLEDIIKQGVNDIIV"
9284. .10159
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9284. .10159
/gene="SPO13"
/note="YHR014W"
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/protein_id="AAB68941.1"
/db_xref="GI:500706"
/translation="MAPRRKRLLEIGSPTHSKKVKVQKLOEKTPLRVSPFLAKICK
EIKKKEIKTKTESNIFNSKHYDLRESHPGLNVSQDQYSKADRYLKKKS
NTLNNRQITIERPSFNSLRFDIEQPKSTSTVLQSQINVEREAPMPVYILA
PSPMVNSPYNFVGNPFLTPSGNPINVAIPIQRELLVYNNVVDSPFKTRLP
HOTKSLDKKKYQYLPIYPVSIISNNQFVGQETPRAAPKLKSKRLSTLIDVNCSDYES
SGCATYNDSSSLN"
complement (10264. .10345)
/gene="TS (AGA)H"
complement (10264. .10345)
/gene="TS (AGA)H"
/product="CRNA-Ser"
/note="codon recognized: UCU"
10911. .11246
/note="delta element"
11559. .11630
/gene="TQ (UUG)H"
11559. .11630
/gene="TQ (UUG)H"
/product="CRNA-Gln"
/note="codon recognized: CAA"
11791. .13770
/gene="YHR015W"
11791. .13770
/gene="YHR015W"
/note="similar to polyadenylate-binding protein in
N-terminus."
/codon_start=1
/evidence=not experimental
/product="Yhr015Wp"
/protein_id="AAB68942.1"
/db_xref="GI:500707"
/translation="WPNHGNYLNNISLNSKQNPSSISKSCNDKADAKSKTKTISAO
ALVRVQAGYKLDGKDAVEKENSILKKYDCKNATQEKQEOVEFEYTAQSGVOK
YITKTSKNSLFIQNLKSTVTEEMLRKIFKRYQSFESAQVCRDPLTKKSLGYINFK

Alignment Scores:
Pred. No.: 1.09e-06 Length: 18715
Score: 100.00 Matches: 18
Percent Similarity: 82.14% Conservative: 5
Best Local Similarity: 64.29% Mismatches: 5
Query Match: 68.97% Indels: 0
DB: Gaps: 0
US-09-987-190-2 (1-30) x YSCHL2825 (1-18715)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 751 AAAGTCACCTTGCCAGACTGGAAGTGGAGCTTCGTCATTGGAACCTTATCTCCGGT 692
QY 21 GAlleAsnGluIle**TyrThr 28
Db 691 CAAATCACGATTTGCATTTCACC 668
RESULT 13
YSC9780/c 24431 bp DNA linear PLN 03-SEP-1997
LOCUS Saccharomyces cerevisiae chromosome VIII cosmid 9780.
DEFINITION U10555 U00093
ACCESSION U10555.1 GI:500813
VERSION
KEYWORDS
SOURCE
ORGANISM
Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE
AUTHORS
1 (bases 1 to 24431)
Johnston,M., Andrews,S., Brickman,R., Cooper,J., Ding,H., Dover,J.,
Du,Z., Favellio,A., Fulton,L., Gattung,S., Giesel,C., Kirsten,U.,
Kucaba,T., Hillier,L., Jier,M., Johnston,L., Keppler,D.,
Langston,Y., Latreille,P., Lewis,E., Macri,C., Mardis,E.,
Mouser,L., Nhan,M., Rifken,L., Riley,L., St.Peter,H., Thornton,L.,
Trevaaskis,E., Vaudin,M., Vaughan,K., Vignati,D., Wilcox,L.,
Wills,A., Wilson,R., Woldman,P. and Waterston,R.
Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
VIII
JOURNAL
MEDLINE
94378003
8091229
2 (bases 1 to 24431)
Favellio,T.
The sequence of S. cerevisiae cosmid 9780
unpublished (1994)
REFERENCE
AUTHORS
JOURNAL
TITL
3 (bases 1 to 24431)
Waterston,R.
Direct Submission
JOURNAL
REFERENCE
4 (bases 1 to 24431)
Jia,Y. and Cherry,J.M.
Direct Submission
Submitted (03-SEP-1997) Department of Genetics, Stanford
University, Saccharomyces Genome Database, Stanford, CA 94305-5120,
USA
COMMENT
Curated by:
Saccharomyces Genome Database
URL: http://genome-www.stanford.edu/
e-mail: yeast-curator@genome.stanford.edu
Submitted by:
Genome Sequencing Center
Department of Genetics, Washington University,
St. Louis, MO 63110, USA
e-mail: mj@sequencer.wustl.edu
NEIGHBORING COSMID INFORMATION:
This sequence includes nucleotides 10590-34824 of cosmid 9780. The
adjacent clone on the right is YSCHL2825. The adjacent clone on

LIPADBSPTFTVDCJDNLESKYDLLEAHNNKIDVISSMGVATKSDPTRVSIINDISM

Alignment Scores:

Pred. No.: 1,51e-06 Length: 24431
 Score: 100.00 Matches: 18
 Percent Similarity: 82.14% Conservative: 5
 Best Local Similarity: 64.29% Mismatches: 5
 Query Match: 68.97% Indels: 0
 DB: 8 Gaps: 0

US-09-987-190-2 (1-30) x YSGH9780 (1-24431)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPhseSerAlaThrGluProTyrIleSerGly 20

Db 24382 AAAGTCACTTGCCGACCTTGAACTGGGACCTTCGCTGATTGGAACCTTATATCTCCGGT 24323

Qy 21 GlnIleAsnGluIle***TyrThr 28

Db 24322 CAATCAACGAGATTGCATTACACC 24299

RESULT 14

AF061031

LOCUS

Mycobacterium smegmatis superoxide dismutase (sodA) gene, complete cds; and unknown gene.

DEFINITION

AF061031 GI:15724846

VERSION

KEYWORDS

SOURCE

ORGANISM

Mycobacterium smegmatis
Mycobacterium smegmatis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Mycobacteriaceae; Mycobacterium.

1 (bases 1 to 1071)

Hartsh.G. and Horwitz,M.A.

Export of recombinant Mycobacterium tuberculosis superoxide

dismutase is dependent upon both information in the protein and

mycobacterial export machinery. A model for studying export of

leaderless proteins by pathogenic mycobacteria

J. Biol. Chem. 274 (7), 4281-4292 (1999)

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

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JOURNAL

MEDLINE

REMARK COMMENT

FEATURES

source

1..1071

/organism="Mycobacterium smegmatis"

/mol_type="genomic DNA"

/strain="1-2c"

/db_xref="taxon:1772"

41..141

/note="similar to partialorf adjacent to Mycobacterium

fortitulum soda gene"

/codon_start=1

/transl_table=11

gene

CDS

/product="unknown"

/protein_id="AA06643.1"

/db_xref="GI:15724848"

/translation="SSGSALPQPEHNTSGHLQTRHQVAFLRACVIAAILLGLAVIF

WF"

282..905

/gene="soda"

282..905

/gene="soda"

/EC_number="1.15.1.1"

/codon_start=1

/transl_table=11

/product="superoxide dismutase"

/protein_id="AADI5825.2"

/db_xref="GI:15724847"

/translation="MAEYTPDDVDYDYGALPEPHISGQINELHSHKHATYVKGVNDAL

AKLEBRANDDAIPIUNEKTLAFHIGGHNISIMKNSPNGGDKPTGLAAIDPO

FGSFDKFGQAFITAAANGLOSSGNVAYGYSGLSRLITFOIXDOANVPLGIITPLQVD

MMEHAFYLYQKRVKADYVAFMNVVMDVQNFPAATSKTSGLIFG"

964..996

stem_loop

Alignment Scores:

Pred. No.: 4.76e-08 Length: 1071
 Score: 99.00 Matches: 16
 Percent Similarity: 89.29% Conservative: 9
 Best Local Similarity: 57.14% Mismatches: 3
 Query Match: 68.28% Indels: 0
 DB: 1 Gaps: 0

US-09-987-190-2 (1-30) x AF061031 (1-1071)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPhseSerAlaThrGluProTyrIleSerGly 20

Db 288 GAATACACCTGCGGACCTGATGACGATGAGACCCGACCCCAATATCTCCGGT 347

Qy 21 GlnIleAsnGluIle***TyrThr 28

Db 348 CAGATCAACGAGCTGCACACACG 371

RESULT 15

MFSODA

LOCUS

M.fortitulum sod gene.

DEFINITION

X70914

VERSION

KEYWORDS

SOURCE

ORGANISM

Mycobacterium fortitulum

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Mycobacteriaceae; Mycobacterium.

1

Menéndez,M.C., Domenech,P., Prieto,J. and Garcia,M.J.

Cloning and expression of the Mycobacterium fortitulum superoxide

dismutase gene

FEMS Microbiol. Lett. 134 (2-3), 273-278 (1995)

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REMARK COMMENT

FEATURES

source

1..1478

/organism="Mycobacterium fortitulum"

/mol_type="genomic DNA"

/strain="1-2c"

/db_xref="taxon:1772"

41..141

/note="similar to partialorf adjacent to Mycobacterium

fortitulum soda gene"

/codon_start=1

/transl_table=11

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/mol_type="genomic DNA"
/strain="ATCC 6841"
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243..250
257..880
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257..880
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/transl_table=11
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/protein_id="CA50266.1"
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/db_xref="GOA:Q59519"
/db_xref="SWISS-PROT:Q59519"
/translation="MAEYTLPLDLDYDGLALPHISGQINELHSHKHAAYKGVNDAY
AKLDEARANGHAIPLNEKULAPHLGCHVHNSIMWKULSPGSGDKPTGDIAMAIIDQ
FGSFDKFAQPTAAANGIQSGMAVLGYDLSGDRLLTFQLDQGANVPLGIIPLLQVD
MWEHAFYIQYNKADYKAFWNVNVMEDVONRYAATSKTNGLIFG"

ORIGIN
Alignment Scores:
Pred. No.: 7.09e-08 Length: 1478
Score: 99.00 Matches: 16
Percent Similarity: 89.29% Conservative: 9
Best Local Similarity: 57.14% Mismatches: 3
Query Match: 68.28% Indels: 0
DB: 1 Gaps: 0

US-09-987-190-2 (1-30) x MFSODA (1-1478)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 20
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 263 GAATACACTTGGCCGACCTGATTCAGACTACGAGAGACTGAGAGCCCATCTCGAGG 322
QY 21 GlnIleSngIuile***TyrThr 28
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 323 CAGATCAACGAGCTCCACACAGC 346

RESULT 16
MLEPSSOD 649 bp DNA linear BCT 10-FEB-1999
LOCUS Mycobacterium leprae DNA for manganese superoxide dismutase (bc
1.15.1.1).
X16453
X16453.1 GI:44405
manganese superoxide dismutase; metalloenzyme; superoxide
dismutase.
SOURCE Mycobacterium leprae
ORGANISM Mycobacterium leprae
REFERENCE Actinobacteridae; Actinomycetales;
Corynebacteriinae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 649)
Thangaraj,H.S., Lamb,F.I., Davis,E.O. and Colston,M.J.
Nucleotide and deduced amino acid sequence of Mycobacterium leprae
manganese superoxide dismutase
Nucleic Acids Res. 17 (20), 8378 (1989)
JOURNAL MEDLINE 90045970
PUBMED 2682526
REFERENCE 2 (bases 1 to 649)
Thangaraj,H.S.
TITLE Direct Submision
AUTHORS Submitted (01-SEP-1989) Thangaraj H.S., National Institute for
Medical Research, Laboratory of Leprosy and Mycobacterial Research,
Mill Hill, London NW7 1AA, UK
JOURNAL Location/Qualifiers
1..649
/organism="Mycobacterium leprae"
/mol_type="genomic DNA"
/db_xref="taxon:1769"

FEATURES
source
```

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/clone="Y3164 and pHT7"
/clone_1ib="lambda gcl1 and pHC79 cosmid"
1..4
/note="pot. ribosome binding site"
14..637
/note="unnamed protein product; superoxide dismutase (AA
1-207)"
/codon_start=1
/transl_table=11
/protein_id="CA34472.1"
/db_xref="GI:581343"
/db_xref="GOA:P13367"
/db_xref="SWISS-PROT:P13367"
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AKLDEARAKDHSALPLNEKULAPHLGCHVHNSIMWKULSPGSGDKPTGDIADIDET
FGSFDKFAQPSAANGIQSGMAVLGYDLSGDRLLTFQLDQGANVPLGIIPLLQVD
MWEHAFYIQYNKADYKAFWNVNVMADVOSRYAATSKTNGLIFD"

ORIGIN
Alignment Scores:
Pred. No.: 3.89e-08 Length: 649
Score: 98.00 Matches: 16
Percent Similarity: 92.86% Conservative: 10
Best Local Similarity: 57.14% Mismatches: 2
Query Match: 67.59% Indels: 0
DB: 1 Gaps: 0

US-09-987-190-2 (1-30) x MLEPSSOD (1-649)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 20
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 GAATACACCTTGGCCGACCTGATTCAGACTACGAGAGCTGAGAGCCCATCTCTGCT 79
QY 21 GlnIleSngIuile***TyrThr 28
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 GAGATCAACGAGATCCACACAGC 103

RESULT 17
MLEPRTN/c 344050 bp DNA linear BCT 20-FEB-2001
LOCUS Mycobacterium leprae strain TN complete genome; segment 1/10.
ACCESSION AL583917 AL450380
VERSION AL583917.1 GI:13092412
KEYWORDS
SOURCE
ORGANISM Mycobacterium leprae
Mycobacterium leprae
Bacteria; Actinobacteridae; Actinobacteriidae; Actinomycetales;
Corynebacteriinae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 344050)
Cole,S.T., Bigmeier,K., Parkhill,J., James,K.D., Thomson,N.R.,
Wheeler,P.R., Honore,N., Ganter,T., Churcher,C., Harris,D.,
Mungall,K., Basham,D., Brown,D., Chillingworth,T., Connor,R.,
Davies,R.M., Devlin,K., Dutfoy,S., Feltwell,T., Fraser,A.,
Hamlin,N., Holroyd,S., Hornsby,T., Jagels,K., Lacroix,C.,
Maclean,J., Moule,S., Murphy,L., Oliver,Quail,M.A.,
Rajandream,M.-A., Rutherford,K.M., Rutter,S., Seeger,K., Simon,S.,
Simmonds,M., Skelton,J., Squares,R., Squares,S., Stevens,K.,
Taylor,K., Whitehead,S., Woodward,J.R. and Barrell,B.G.
Massive gene decay in the leprosy bacillus
Nature 409 (6823), 1007-1011 (2001)
JOURNAL MEDLINE 21128732
PUBMED 11234002
REFERENCE 2 (bases 1 to 344050)
Parkhill,J.
TITLE Direct Submision
AUTHORS Submitted (20-FEB-2001) Submitted on behalf of the Mycobacterium
leprae sequencing teams, The Sanger Centre, Wellcome Trust Genome
Campus, Hinxton, Cambridge, CB10 1SA, UK Unite de Genetique
Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux,
75724, Paris Cedex, France. E-mail: parkhill@sanger.ac.uk
COMMENT
Notes:
Details of M. leprae sequencing at the Sanger Centre are available
from http://www.sanger.ac.uk/Projects/M_leprae/ A relational
```

FEATURES

database containing the M. leprae sequences is available from
http://genolist.pasteur.fr/Leprae/.

Location/Qualifiers

1. 344050

/organism="Mycobacterium leprae"

/mol_type="genomic DNA"

/strain="TN"

/db_xref="taxon:1769"

gene

1. 1566

CDS

/note="synonym: ML0001"

CDS

1. 1566

CDS

/note="Similar to M. tuberculosis dnaA, chromosomal replication initiator protein, SW:DNA_MYCTU (P49993) (507 aa); Fasta score E(): 0, 87.2% identity in 507 aa overlap and Mycobacterium smegmatis dnaA, SW:DNA_MYCSM (P49992) (495 aa); Fasta score E(): 0, 69.2% identity in 441 aa overlap. Previously sequenced as SW:DNA_MYCLE (P46388) (521 aa); Fasta score E(): 0, 99.8% identity in 521 aa overlap. Contains Pfam match to entry PF00308 bac_dnaA, Bacterial dnaA protein. Contains PS00017 ATP/GTP-binding site motif A (P-loop). Contains PS01008 dnaA protein signature."

/codon_start=1
/transl_table=1
/product="putative chromosomal replication initiator protein"
/protein_id="CAC29509.1"
/db_xref="GI:13092413"
/db_xref="GOA:P46388"
/db_xref="SWISS-PROT:P46388"
/translation="MEVPHAKPEITYNQORDTSLADLSIGFTTWMNAVSEUNGESN TDEATNDSTLVPLPQORAMNLVPLTIEGFALLSPSSFVQNEIEHLKPTT DALSRLGQOIQGVRIAPSTDIIDNSSADVLINDGCTIDENYGEPLTGEYOG LPYFTRPHHTSEITVGTGSLNRYTEFEVIGASNRFAAALAIADAEAPAKANPL FIMESGIGKTHILHAAGNAQORLPQGRVYKVTSEETPNDPINSLRDPRVAKRSY RDVVLIVDDIQFIEGKEGIOEFPHNTLNANKQIVISSDRPPKQALTEERLRT RFEGMLITDVPPELETRIALRKKAQMERLAVGDVLELASEIENKELBEALIR VTAASLNTKAIIDKALAEIVRLIDASTVQISATITMTATYFPTTIEELGPBK TRALASROIAMYLCRELIDSLPKIQAFGRDHTTWYAKRKILSEMAERREVFHY KELTRIRORSKR"

544. 1482
/gene="dnaA"
/note="Pfam match to entry PF00308 bac_dnaA, Bacterial dnaA protein, score 712.20, E-value 8.3e-240"

664. 687
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/note="PS00017 ATP/GTP-binding site motif A (P-loop)"

1426. 1482
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/note="PS01008 DnaA protein signature"

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/protein_id="CAC29512.1"
/db_xref="GI:13092416"
/db_xref="SWISS-PROT:Q9CDF4"
/translation="MIESNYSYGDDTPEPTLGSFPLVRRALFEARAAACAGKD
AGRGVVPVPRVTRDRNRNMGPGDPDVPDPLAKKRGKSAQAEGVFG
QMAWVGQIADHAFPGVGNVSLVTAESTIMATQRLIMQKLIATAAAGNGVVT
SIKITPTAPSRKRPWHIAGRPDTYG"
RBS
5211..5216
/note="possible RBS"
5229..7265
/gene="gyrB"
/note="synonym: ML0005"
5229..7265
/gene="gyrB"
/EC_number="5.99.1.3"
/note="Similar to M. tuberculosis gyrB, DNA gyrase subunit
B, SW:GYRB MYCTU (P4514) (686 aa); Fasta score E() = 0,
87.5% identity in 679 aa overlap and to Mycobacterium

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Alignment Scores:

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Pred. No.: 9.3e-05 Length: 344050
Score: 98.00 Matches: 16
Percent Similarity: 92.86% Conservative: 10
Best Local Similarity: 57.14% Mismatches: 2
Query Match: 67.59% Indels: 0
DB: 1 Gaps: 0

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US-09-987-190-2 (1-30) x MLEPRTN1 (1-344050)

QY 1 LysTyrSerLeuPProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

Db 93264 GAATACACCCCTGGCGATTGGAGCTACGACGCTGGAACGACATATCTCGGT 93205

QY 21 GlnIleAsnGluIle***TyrThr 28

Db 93204 GAGATCAACGAGATCCACACACC 93181

RESULT 18

MTSOD

LOCUS M.tuberculosis SOD gene. 790 bp DNA linear BCT 03-MAY-1995
 ACCESSION X52861
 VERSION X52861.1 GI:794079
 KEYWORDS sod gene; superoxide dismutase.
 SOURCE Mycobacterium tuberculosis
 ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Mycobacteriaceae; Mycobacteriidae; Mycobacterium; Mycobacterium
 tuberculosis complex.
 1 (bases 1 to 790)
 Zhang, Y., Lathigra, R., Garbe, T., Gatty, D. and Young, D.
 Genetic analysis of superoxide dismutase, the 23 kilodalton antigen
 of Mycobacterium tuberculosis
 JOURNAL M.O. Microbiol. 5 (2), 381-391 (1991)
 MEDLINE 91251768
 PUBMED 1904126
 2 (bases 1 to 790)
 Zhang, Y.
 Direct Submission
 Submitted (23-APR-1990) Zhang Y., MRC TB & Related Infections Unit,
 Cyclotron Bldg, Hammersmith Hospital, London W12 0HS, U K
 On May 4, 1995 this sequence version replaced gi:44678.
 Data kindly reviewed (02-JUL-1990) by Zhang Y.
 Related sequence: S36714
 Location/Qualifiers
 1..790
 /organism="Mycobacterium tuberculosis"
 /mol_type="genomic DNA"
 /strain="H37RV"
 /db_xref="taxon:1773"
 /clone="YA3P-9"

FEATURES

source

-35_signal

/clone_1ib="lambda gt11"
 20..25
 /note="putative"

RBS

99..105
 /gene="SOD"

gene

112..735
 /gene="SOD"

112..735
 /gene="SOD"

CDS

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/EC_number="1.15.1.1"
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/translation_except=(pos:112..114,aa:Met)
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/protein_id="CAA37042.1"
/db_xref="GI:581379"
/db_xref="GOA:P17670"
/db_xref="SWISS-PROT:P17670"
/translation="MAEYTLPLDMVDYGALEPHISQINELHSHKHATYYKANDAV
AKLEEARAKEDHSAIILNENKILAFNLAGVHTIWMKSLSPNGDKPFGELAAATADA
FGSPDKFPAQPHAAATVQSGMAALGMDTLGNKLLIFOYVDHOTNPLGLIVPLILLD
MMEHAFYLQYKNVAVDFAKAFNNVNMADVDSRYAAATSOTKGLIFG"

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Alignment Scores:

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Pred. No.: 2.66e-07 Length: 790
Score: 94.00 Matches: 15
Percent Similarity: 89.29% Conservative: 10
Best Local Similarity: 53.57% Mismatches: 3
Query Match: 64.83% Indels: 0
DB: 1 Gaps: 0

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US-09-987-190-2 (1-30) x MTSOD (1-790)

QY 1 LysTyrSerLeuPProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

Db 118 GAATACACCTTGCAGACCTGAGCTGAGACTACGAGACGACGACGACATCTCGGT 177

QY 21 GlnIleAsnGluIle***TyrThr 28

Db 178 GAGATCAACGAGCTTCCACACACC 201

RESULT 19

AF077406

LOCUS AF077406 943 bp DNA linear BCT 26-JUL-1998
 DEFINITION Mycobacterium bovis BCG superoxide dismutase (SOD) gene, complete
 ACCESSION AF077406 GI:3342171
 VERSION AF077406.1
 KEYWORDS

SOURCE Mycobacterium bovis BCG
 ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacteriaceae; Mycobacteriaceae; Mycobacterium; Mycobacterium
 tuberculosis complex.
 1 (bases 1 to 943)
 Kimble, E., Sanderson, R.J. and Gill, R.E.
 Superoxide dismutase of M. bovis BCG
 JOURNAL Unpublished
 2 (bases 1 to 943)
 Kimble, E., Sanderson, R.J. and Gill, R.E.
 Direct Submission
 Submitted (10-JUL-1998) Microbiology, University of Colorado Health
 Sciences Center, 4200 E. 9th Ave., Denver, CO 80220-3706, USA
 Location/Qualifiers
 1..943
 /organism="Mycobacterium bovis BCG"
 /mol_type="genomic DNA"
 /strain="Pasteur"
 /db_xref="taxon:33892"
 /gene="SOD"
 307..943
 /gene="SOD"
 307..314
 /gene="SOD"

FEATURES

source

CDS

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/note="putative"
320..943
/feature="SOD"
/note="similar to Mycobacterium tuberculosis superoxide
dismutase encoded by the sequence presented in GenBank
Accession Number X52861"
/codon_start=1
/transl_table=11
/product="superoxide dismutase"
/protein_id="AAC27527.1"
/db_xref="GI:3342172"
/translation="MAEYTLPLDMDYGALEPHISQINELHSHKHATYVKANDAV
AKLEBARAKEDHSAIILNEKNLAFNLAGVNHITIMKNLSPNGDKPTGELAADA
FGSPDKRRAQFHAATTVQSGMALGMDTLGNKLLILOYDHQTNPLGIVPLLLD
MMEHAFIQLQKVKVDFAKAFNVVWVADVQSRVAAATSTQKGLIFG"
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ORIGIN

Alignment Scores:

Pred. No.:	3,31e-07	Length:	943
Score:	94.00	Matches:	15
Percent Similarity:	89.29%	Conservative:	10
Best Local Similarity:	53.57%	Mismatches:	3
Query Match:	64.83%	Indels:	0
DB:	1	Gaps:	0

US-09-987-190-2 (1-30) x AF077406 (1-943)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrTlleSerGly 20

Db 326 GAATPACACCTTGCCAGACTGCGACTGAGACTGAGACGACGACGACGACATCTCGGGT 385

QY 21 GlnIleasnGluIle***TyrThr 28

Db 386 CAGATCAACGAGCTTCACACAGC 409

RESULT 20

LOCUS AF061030 1321 bp DNA linear BCT 03-MAR-1999

DEFINITION Mycobacterium tuberculosis superoxide dismutase (sodA) gene,

ACCESSION AF061030

VERSION AF061030.1 GI:4321775

SOURCE Mycobacterium tuberculosis

ORGANISM Mycobacterium tuberculosis

REFERENCE 1 (bases 1 to 1321)

AUTHORS Harth,G. and Horwitz,M.A.

TITLE Export of recombinant Mycobacterium tuberculosis superoxide dismutase is dependent upon both information in the protein and mycobacterial export machinery. A model for studying export of leaderless proteins by pathogenic mycobacteria

JOURNAL J. Biol. Chem. 274 (7), 4281-4292 (1999)

MEDLINE 99134360

PUBMED 9933629

REFERENCES 2 (bases 1 to 1321)

AUTHORS Harth,G. and Horwitz,M.A.

TITLE Direct Submission

JOURNAL Submitted (23-APR-1998) Medicine, UCLA, 10833 Le Conte Avenue, Los Angeles, CA 90095, USA

FEATURES

source

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/organism="Mycobacterium tuberculosis"

/mol_type="genomic DNA"

/strain="Brdman"

/db_xref="taxon:1773"

542..1165

/gene="soda"

542..1165

/gene="soda"

/EC_number="1.15.1.1"

CDS

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AKLEBARAKEDHSAIILNEKNLAFNLAGVNHITIMKNLSPNGDKPTGELAADA
FGSPDKRRAQFHAATTVQSGMALGMDTLGNKLLILOYDHQTNPLGIVPLLLD
MMEHAFIQLQKVKVDFAKAFNVVWVADVQSRVAAATSTQKGLIFG"
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ORIGIN

Alignment Scores:

Pred. No.:	5.03e-07	Length:	1321
Score:	94.00	Matches:	15
Percent Similarity:	89.29%	Conservative:	10
Best Local Similarity:	53.57%	Mismatches:	3
Query Match:	64.83%	Indels:	0
DB:	1	Gaps:	0

US-09-987-190-2 (1-30) x AF061030 (1-1321)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrTlleSerGly 20

Db 548 GAATPACACCTTGCCAGACTGCGACTGAGACTGAGACGACGACGACATCTCGGGT 607

QY 21 GlnIleasnGluIle***TyrThr 28

Db 608 CAGATCAACGAGCTTCACACAGC 631

RESULT 21

LOCUS AX708732 1321 bp DNA linear PAT 04-APR-2003

DEFINITION Sequence 57 from Patent WO02074991.

ACCESSION AX708732

VERSION AX708732.1 GI:29564462

SOURCE Mycobacterium tuberculosis

ORGANISM Mycobacterium tuberculosis

REFERENCE 1

AUTHORS Karlzen,F.

JOURNAL Detection of microorganisms using inducible genes

Patent: WO 02074991-A 57 26-SEP-2002;

Norchip A/S (NO)

FEATURES

source

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/organism="Mycobacterium tuberculosis"

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/db_xref="taxon:1773"

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/note="unnamed protein product"

/codon_start=1

/transl_table=11

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/db_xref="GI:29564463"

/db_xref="REMBTREMBL:CAD88162"

/translation="MAEYTLPLDMDYGALEPHISQINELHSHKHATYVKANDAV

AKLEBARAKEDHSAIILNEKNLAFNLAGVNHITIMKNLSPNGDKPTGELAADA

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MMEHAFIQLQKVKVDFAKAFNVVWVADVQSRVAAATSTQKGLIFG"

Alignment Scores:

Pred. No.:	5.03e-07	Length:	1321
Score:	94.00	Matches:	15
Percent Similarity:	89.29%	Conservative:	10
Best Local Similarity:	53.57%	Mismatches:	3
Query Match:	64.83%	Indels:	0
DB:	6	Gaps:	0

US-09-987-190-2 (1-30) x AX708732 (1-1321)

	Qy	LvsITyrSerLeuProGluIleuaspsPyrGiunPheserAlAThGlubProfYrllSeSergly :: Db
	548	GAAATACCTTCGCAGACTGGAGCTCGGAAGAACAAGCACTGCCAATCCTCCGT 607
	Qy	21 GlnIleaSnGuile**TyrThr 28 :: Db
	608	CAGATTCAAAGACTTCACCACAGC 631
	RESULT 22	
	AEO07188	14282 bp DNA linear BCT 27 APR-2001
	LOCUS	Mycobacterium tuberculosis CDCt155l, section 274 of 280 of the complete genome.
	ACCESSION	AE007188 AE009516
	VERSION	AE007188.1 GI:1383836
	SOURCE	Keywords:
	ORGANISM	Mycobacterium tuberculosis CDCt155l Mycobacterium tuberculosis CDCt155l Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales; Corynobacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex. 1 (bases 1 to 14282) Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O., Peterson,J.F., Deboy,R., Dodson,R., Grimm,M., Haft,D., Hickey,E., Kolonay,T.J., Nelson,W.C., Umayan,L.A., Ermolaeva,M., Salzberg,S.L., Delcher,A., Utterback,I., Weidman,J., Khouri,H., Gill,J., Mikula,A. and Bishop,W. Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains unpublished 2 (bases 1 to 14282)
TITLE	JOURNAL	Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O., Peterson,J.F., Deboy,R., Dodson,R., Grimm,M., Haft,D., Hickey,E., Kolonay,T.J., Nelson,W.C., Umayan,L.A., Ermolaeva,M., Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H., Gill,J., Mikula,A. and Bishop,W. Direct Submission Submitted (25-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
TITLE JOURNAL	REFERENCE AUTHORS	Location/Qualifiers 1..14282 /organism="Myco bac terium tuberculo s is CDCt155l" /mol_type="genom i c DN A " /strain="CDCt155l" /db_xref="taxon:83331" /note="clinical strain"
FEATURES	source	130..675 /gene="MT13949" 130.. .675 /gene="MT13949" /note="similar to GB:AEO00666, identified by sequence similarity; putative" /codon_start=1 /transl_table=1 /product="ferritin family protein" /protein_id="AAK48316.1" /db_xref="GI:1383837"
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	gene	
	CDS	

gene
CDS

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complement(1520..2548)
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/protein_id="AAK48318.1"
/db_xref="GI:13883839"
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PARPVPTSDTRRTPPPPLPGSRGTIAVRPGAAPPFRRGRPLRGTPPYAGIPIKGLIL
DHVDQA PVASAKAGSPRAAVRTTLIVSLIFSINVVFLVTNNRTLLPVLNLT
ASASVGLSVLSAIIAAGTTIVLVSMIVARAAAFHQGDPERRSARLIMAGCIL
PMWNLIMALVIYLIELVEDRYTRLRLRPITVMWIIVISNAISMFAFTSVTDAGOG
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gene
CDS

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/translation="MDNSARQCVLIDSLAGRAKMIVALSTHICGCT"
3087..3236
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/transl_table=11
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/protein_id="AAK48320.1"
/db_xref="GI:13883841"
/translation="MATHSYGPGSTTPPNSSGPENMNAVGIALLRALIMALLAILIA
VIALY"

gene
CDS

complement(3637..3849)
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/note="identified by Glimmer2; putative"
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/protein_id="AAK48321.1"
/db_xref="GI:13883842"
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EFGACAVAGRAIRPGLSDBAAQYNQ"
complement(4199..4801)
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/protein_id="AAK48322.1"
/db_xref="GI:13883843"
/translation="MTGRRRVSDSDPDPAWSMILGSHGLATLCMEVLPITYNNVUL
MKSSRIIGPQPPIYRELIYA VGEPSTALPAQLPHHPRPQSGSSRAALVLDSDNH
SKRRCCALPQHGPFKEQFRQSWSSRAQTLSKRRAALOPLRRPPLYLTTP
SKRIKKYKPKPAGSGPRLEDQPVCLLTLLFAFKQVP"

gene
CDS

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complement(1520..2548)
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/protein_id="AAK48318.1"
/db_xref="GI:13883839"
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PARPVPTSDTRRTPPPPLPGSRGTIAVRPGAAPPFRRGRPLRGTPPYAGIPIKGLIL
DHVDQA PVASAKAGSPRAAVRTTLIVSLIFSINVVFLVTNNRTLLPVLNLT
ASASVGLSVLSAIIAAGTTIVLVSMIVARAAAFHQGDPERRSARLIMAGCIL
PMWNLIMALVIYLIELVEDRYTRLRLRPITVMWIIVISNAISMFAFTSVTDAGOG
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LDGEPRDA"

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CDS       4727. 5218
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          similarity; putative"
          /codon_start=1
          /transl_table=11
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          LAGRTTDLKSGDDIDATVPTSMWLTTLTAVENAGDTMAGARHCARLGATV
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          LAR"
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          /complement(5255. 5797)
          /gene="MT3957"
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          /db_xref="GI:13883845"
          /translation="MGI:SKTIPRCRPSLPIVGRGRPSLRGDSITVTPCSPTMGSK
          EPKMETASSDRVCYNRIPCRQMSACRFLVHGVSVGAVYVGVVDVVGQDQFR
          AAGDRAVGVAGLVGAAGDRHPGAFGLAGDGLGVAMPGLGHPVVERQVAG
          RCAGQADVGPTPOHRCRGR"
          5778. 5993
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          5778. 5993
          /gene="MT3958"
          /note="identified by Glimmer2; putative"
          /codon_start=1
          /transl_table=11
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          /protein_id="AAK48325.1"
          /db_xref="GI:13883846"
          /translation="MVPDKPTVSCLSVSHFORLFRVAOHNPVEYIRRDYHTQHLH
          RDSGRRLTSSFAPPAATQHRGSS"
          complement(6207. 6386)
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          /note="identified by Glimmer2; putative"
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          /db_xref="GI:13883847"
          /translation="WMRRSGMVGKKSTAGQLAGTANELTKREIVRAVHESPIVR
          DVVVGIPAVDRRPKQ"
          6657. 7280
          /gene="MT3960"
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          /note="similar to SP:P47201 PID:555746 PID:620090
          PID:667039 SP:P53647; identified by sequence similarity;
          putative"
          /codon_start=1
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          /db_xref="GI:13883848"

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Alignment Scores:

Score:	Length:
9.63e-06	14282
94.00	15
89.29%	10
53.57%	3
64.83%	0

DB: 1 Gaps: 0

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US-09-987-190-2 (1-30) x AE007188 (1-14282)
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Db      6663 GAATACACCTTGCCACCTGCGACTGACGACCTGACACCGCACATCTCGGT 6722
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      21 GlnIleAsnGluIle**TyrThr 28
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Db      6723 CAGATCAACGAGCTTCACCAACAGC 6746
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RESULT 23
BX842584      244800 bp      DNA      circular BCT 21-NOV-2003
Mycobacterium tuberculosis H37Rv complete genome; segment 13/13.
LOCUS      BX842584 AL021426 AL022076 AL022120 AL123456 280343 283864
DEFINITION      294121 297188
ACCESSION      BX842584.1 GI:38490370
VERSION      complete genome.
KEYWORDS      Mycobacterium tuberculosis H37Rv
SOURCE      Mycobacterium tuberculosis H37Rv
ORGANISM      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
      Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
      tuberculosis complex.
REFERENCE
  1 Cole,S.T., Brosch,R., Parkhill,J., Garnier,T., Churcher,C.,
    Harris,D., Gordon,S.V., Eigemeier,K., Gas,S., Barry III,C.E.,
    Tekala,F., Badcock,K., Basham,D., Brown,D., Chillingworth,T.,
    Connor,R., Davies,R., Devlin,K., Feltwell,T., Gentile,S.,
    Hamlin,N., Holroyd,S., Hornsby,T., Tagatz,K., Krogh,A., McLean,J.,
    Moule,S., Murphy,L., Oliver,S., Osborne,J., Quail,M.A.,
    Rajandream,M.A., Rogers,J., Rutter,S., Seeger,K., Skellon,S.,
    Squares,S., Squires,R., Stulson,J.E., Taylor,K., Whitehead,S. and
    Barrrell,B.G
    Deciphering the biology of Mycobacterium tuberculosis from the
    complete genome sequence
    Nature 393 (6685), 537-544 (1998)
    PUBMED 98295987
    JOURNAL 9634230
  2 Camus,J.C., Pryor,M.J., Medigue,C. and Cole,S.T.
    Re-annotation of the genome sequence of Mycobacterium tuberculosis
    H37Rv
    Microbiology (Reading, Engl.) 148 (Pt 10), 2967-2973 (2002)
    JOURNAL 12368430
    MEDLINE 22255591
    PUBMED 12368430
    JOURNAL 3 (bases 1 to 244800)
    REFERENCE Parkhill,J.
    TITLE Direct Submission
    JOURNAL Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
    tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome
    Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique
    Moleculaire Bacterienne, Institut Pasteur, 28 rue Du Docteur Roux,
    75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
    On or before Nov 21, 2003 this sequence version replaced
    gi:3261511, gi:3256026, gi:3261558, gi:3261559, gi:3261648,
    gi:3261687, gi:3261736, gi:3261805.
    Notes:
    Details of M. tuberculosis sequencing at the Sanger Centre are
    available on the World Wide Web.
    (URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/).
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      /function="UNKNOWN"
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hypotheoretical protein, equivalent to 069513|MLCB2407.14 (alias 09CB73|ML2336, 463 aa) HYPOTHETICAL 46.8 KDA PROTEIN from *Mycobacterium leprae* (426 aa), FASTA scores: opt: 2505, E(): 8.3e-154, (87.25% identity in 424 aa overlap). Also highly similar to 09RUI7|DR1579 CONSERVED HYPOTHETICAL PROTEIN from *Deinococcus radiodurans* (452 aa), FASTA scores: opt: 1162, E(): 3.1e-67, (44.8% identity in 422 aa overlap); and partially similar to 09I371|PA1654 PROBABLE AMINOTRANSFERASE from *Pseudomonas aeruginosa* (388 aa) FASTA scores: opt: 162, E(): 0.0078, (25.85% identity in 348 aa overlap) and other aminotransferases. Tblast score is 0.900. N-terminus extended since first submission (previously 408 aa)."

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DGPVDLIEELVADPAIKGMWVVFNGSGVSMETVRIMOMRTAAPDFMD
NAYAVHTLIDPEPROVDYGLAAKAGNPNRPYVASTSKITPAGGVSFPGSLGNTA
WYLGAGKSTIGDKNKNQRLHRRFGADSYRLHMQQLARFALVAELDQRLS
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IABSPSYVDLKNVVDGLATCALAAETILLNOGLASSAPNVR"

1613.1698
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1613.1698
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/note="codon recognized: UCC"
/anticodon={pos:1647..1649,aa:Ser}
1804.2568
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1804.2568
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/function="UNKNOWN"
/note="RV3723, (MTV025.071), len: 254 aa. Probable conserved transmembrane protein, with hydrophobic stretches at the N-terminus, and equivalent to 069512|ML2337|MLCB2407.13c PUTATIVE MEMBRANE PROTEIN from *Mycobacterium leprae* (250 aa), FASTA scores: opt: 1029, E(): 1.2e-44, (64.45% identity in 253 aa overlap). Tblast score is 0.900."
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KTKAKDEAPPEAEBENTELAAQEBEVEVPPESIESPGESPESATEAVALFTA
TAEPREGGLRNRPPTGKTSRRRRRSGVAVAVDE"

2735.2977
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2735.2977
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2735.2977
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/function="HYDROLYSIS OF CUTIN (A POLYESTER THAT FORMS THE STRUCTURE OF PLANT CUTICLE)."
/note="RV3724A, (MTV025.072), len: 80 aa. Probable cut5a, truncated cutinase precursor (EC 3.1.1.-), similar to N-terminal end of others e.g. 09XK87 SERINE ESTERASE CUTINASE from *Mycobacterium avium* (220 aa), FASTA scores: opt: 202, E(): 1.5e-06, (56.45% identity in 62 aa overlap); 09XB09|RV2-RV1758 PROTEIN (FRAGMENT) from *Mycobacterium bovis* BCG (143 aa), FASTA scores: opt: 200, E(): 1.5e-06, (61.4% identity in 57 aa overlap); and

000298|CUTI BOTCI|CUTA CUTINASE PRECURSOR from *Botrytis cinerea* (Botryotinia fuckeliana) (202 aa) FASTA scores: opt: 108, E(): 2.2, (40.4% identity in 52 aa overlap). Also highly similar to others from *Mycobacterium tuberculosis* e.g.
006318|CUT3 MYCTU|RV3451|MT3557|MTCY13E12.04 PROBABLE CUTINASE PRECURSOR (247 aa), FASTA scores: opt: 189, E(): 1.2e-05, (58.0% identity in 50 aa overlap);
050664|CUTP MYCTU|RV2301|MT3558|MTCY339.08c PROBABLE CUTINASE PRECURSOR (219 aa), FASTA scores: opt: 172, E(): 0.00015, (59.2% identity in 49 aa overlap);
006793|RV1758|MTCY28.24|Z95890 HYPOTHETICAL 17.9 KDA PROTEIN (174 aa), FASTA scores: opt: 641, E(): 2.7e-29, (57.2% identity in 166 aa overlap);
006319|RV3452|MTY13E12.05, and U00015.11 from *Mycobacterium leprae*. BELONGS TO THE CUTINASE FAMILY. Rest of cutinase ORF continues as RV3724B|CUT5B, frameshifting could occur near position 4169668. Sequence has been checked but no errors found."
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/protein_id="CAE55632.1"
/db_xref="GI:38490372"

/translation="MDVIRMARRLAAVAGTAATTPGLLSAHVPMWSAECPDEVV
FARCTGPPGIGSGVGLFVDALRPPGRQVTRGLRR"

2874.3437
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2874.3437
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/EC_number="3.1.1.-"
/function="HYDROLYSIS OF CUTIN (A POLYESTER THAT FORMS THE STRUCTURE OF PLANT CUTICLE)."
/note="RV3724B, (MTV025.072), len: 187 aa. Probable cut5b, truncated cutinase (EC 3.1.1.-), similar to C-terminal end of others e.g. 09XB09|RV2-RV1758 PROTEIN (FRAGMENT) from *Mycobacterium bovis* BCG (143 aa) FASTA scores: opt: 335, E(): 3.4e-12, (51.25% identity in 92 aa overlap); 09XK87 SERINE ESTERASE CUTINASE from *Mycobacterium avium* (220 aa), FASTA scores: opt: 251, E(): 2.5e-07, (44.05% identity in 168 aa overlap). Also similar to proteins from *Mycobacterium tuberculosis* e.g. 006793|RV1758|MTCY28.24 HYPOTHETICAL 17.9 KDA PROTEIN (174 aa), FASTA scores: opt: 641, E(): 2.5e-29, (57.25% identity in 166 aa overlap); 006319|RV3452|MTCY13E12.05 HYPOTHETICAL 23.1 KDA PROTEIN (226 aa), FASTA scores: opt: 385, E(): 7.5e-15, (46.65% identity in 165 aa overlap);
006318|CUT3 MYCTU|RV3451|MT3557|MTCY13E12.04 PROBABLE CUTINASE PRECURSOR (247 aa), FASTA scores: opt: 307, E(): 1.9e-10, (40.7% identity in 167 aa overlap);
Q10837|CUTI MYCTU|RV1984c|MT2037|MTCY39.35 PROBABLE CUTINASE PRECURSOR (217 aa), FASTA scores: opt: 261, E(): 6.7e-08, (50.9% identity in 169 aa overlap); etc; and U00015.11 from *Mycobacterium leprae*. 5'-end of gene is RV3724A|CUT5A, frameshifting may occur near position 4169668. Tblast score is 0.918."
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/db_xref="GI:38490373"

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SDPKVIVDIGSDAGSHIQSMASCPQTSQVGGYQGAAGVAVTSVAVPPAVQDA
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GNSPVAHGIVAVVAGVGGANPAASRL"

Alignment Scores:
Pred. No.: 0.000327 Length: 244800
Score: 94.00 Matches: 15
Percent Similarity: 89.29% Conservative: 10
Best Local Similarity: 53.57% Mismatches: 3

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gene
CDS
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451 aa, from Mycobacterium tuberculosis strain H37Rv,
(99.8% identity in 451 aa overlap). Probable conserved
transmembrane protein, with Proline rich N-terminus,
similar to Q9XW6|SCE33.17 PUTATIVE INTEGRAL MEMBRANE
PROTEIN from Streptomyces coelicolor (462 aa) FASTA
scores: opt: 730, E(): 2.7e-21, (38.1% identity in 412 aa
overlap)."
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/db_xref="GI:31620458"
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VYVTLIISITLIGFEMPTARGLDI VTGEPDPLTGAVGWSGASGLVSMGLAYLIS
GMVLTIVGRAYGSPPTIVGSAKAKVGRILLATGLILRAQVAVLGLAVIISGVA
AANAEAAALGFPLLLVGVSALYIVLPLPVLIVLRPLVATIRVATIRPAPVPG
FMRYLIGRLLTIVLVGVGSAIAPAPVITVAVTASGVSYVTRLVGATISALGVT
IGQVLTVPFSGAVVLLYTRDRIRIAEFDLVLTGLEAGPAGPAPVESTNDMLTRP
F"
2086..2739
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217 aa, from Mycobacterium tuberculosis strain H37Rv,
(100.0% identity in 217 aa overlap). Probable conserved
membrane protein, similar to Q9XW5|SCE33.18 PUTATIVE
INTEGRAL MEMBRANE PROTEIN from Streptomyces coelicolor
(231 aa), FASTA scores: opt: 419, E(): 1.5e-19, (36.0%
identity in 211 aa overlap). Equivalent to AAK48159 from
Mycobacterium tuberculosis strain CDC1551 (233 aa) but
shorter 16 aa."
/codon_start=1
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2865..3866
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/locus="Mb3716", len: 333 aa. Equivalent to Rv3691, len:
333 aa, from Mycobacterium tuberculosis strain H37Rv,
(100.0% identity in 333 aa overlap). Conserved
hypothetical protein, similar to Q9XW4|SCE33.19 PUTATIVE
SECRETED PROTEIN from Streptomyces coelicolor (387 aa)
FASTA scores: opt: 481, E(): 6e-23, (36.6% identity in 358
aa overlap). Equivalent to AAK81850 from Mycobacterium
tuberculosis strain CDC1551 (381 aa) but shorter 48 aa."
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/protein_id="CAD95902.1"
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 LMKGRIGPLVAEEIPVIRASETEVGRRLVRRARADALRTATLQRLRLIG
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CDS

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 /locus_tag="Mb3717"

/note="Mb3717, moxR2, len: 358 aa. Equivalent to Rv3692, len: 358 aa, from Mycobacterium tuberculosis strain H37Rv, (100.0% identity in 358 aa overlap). Probable moxR2, methanol dehydrogenase regulatory protein, highly similar (generally longer at N-terminus) to Q9KYM3|SCE33.20 PUTATIVE REGULATORY PROTEIN from Streptomyces coelicolor (329 aa), FASTA scores: opt: 1523, E(): 4.2e-74 (70.9% identity in 330 aa overlap); Q9Z538|SC9B2.21c PUTATIVE REGULATORY PROTEIN from Streptomyces coelicolor (332 aa) FASTA scores: opt: 1008, E(): 1.1e-46 (50.8% identity in 313 aa overlap); Q9U267|MOXR-3|PA80848 METHANOL DEHYDROGENASE REGULATORY PROTEIN from Pyrococcus abyssi (314 aa), FASTA scores: opt: 989, E(): 1.1e-45 (50.6% identity in 302 aa overlap); Q9AAM1|CC0566 MOXR PROTEIN from Caulobacter crescentus (323 aa), FASTA scores: opt: 988, E(): 1.3e-45 (52.3% identity in 306 aa overlap); etc. Also similar to O53170|MTV007.26|MOXR|Fv1479 from Mycobacterium tuberculosis (377 aa); and O07392|AF002133.6|MOXR from Mycobacterium avium (309 aa). Also high similarity with several hypothetical bacterial proteins."

gene

CDS

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 AALLEAMEERQVSEVEGPKPLNPFIYVAATONPLEVGTGLOPAQOCDRLKNTVL
 PARDSEIATIDRAHAGFDPDLSINVAAPALAAKRAEVRYHVAENEVIGTIVDI
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5073. .6395
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 5073. .6395
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/note="Mb3718, len: 440 aa. Equivalent to Rv3693, len: 440 aa (alternative start at 41910), from Mycobacterium tuberculosis strain H37Rv, (100.0% identity in 440 aa overlap). Possible conserved membrane protein, similar to Q9KYM2|SCE33.21 PUTATIVE LIPOPROTEIN from Streptomyces coelicolor (436 aa), FASTA scores: opt: 875, E(): 3.3e-46 (56.2% identity in 448 aa overlap); Q9AAM1|CC0567 HYPOTHETICAL PROTEIN from Caulobacter crescentus (437 aa), FASTA scores: opt: 355, E(): 2.3e-14 (30.9% identity in 450 aa overlap); P73233|SLR2013 HYPOTHETICAL 48.5 KDA PROTEIN from Synecocystis sp. strain PCC 6803 (435 aa), FASTA scores: opt: 340, E(): 1.9e-13 (29.7% identity in 438 aa overlap); etc. Equivalent to AAK48162 from Mycobacterium tuberculosis strain CDC1551 (475 aa) but shorter 35 aa. Also similar to other hypothetical proteins from Mycobacterium tuberculosis; MTV014_7, MTV007_27, and MTCY71_36 M."

/codon_start=1
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Alignment Scores:
 Pred. No.:
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0.000383 Length: 278492
 94.00 Matches: 15

Percent Similarity: 89.29%
 Best Local Similarity: 53.57%
 Query Match: 64.83%
 DB: 1
 Gaps: 0

US-09-987-190-2 (1-30) x BX248347 (1-278492)

QY

1 LysTyrSerLeuPProGluIleuAspTyrGluPheSerAlaThrGluProTyrTlleSerGly 20

Db

189983 GAATCACTTCCCGACCTGAGCTGAGCACTACGAGCACTGGAACCGACATCTCGGdT 190042

QY

21 GlnIleAsnGluIle**TyrThr 28

Db

190043 CAGATCAACGAGCTTCACCAACAGC 190066

RESULT 25

PSOD

PSOD 567 bp DNA linear BCT 14-MAR-1996

DEFINITION

P.freudenreichii sod gene (partial).

ACCESSION

X91650.1 GI:1061201

KEYWORDS

sod gene, superoxide dismutase.

SOURCE

Propionibacterium freudenreichii

ORGANISM

Bacteria; Actinobacteria; Actinobacteridae; Propionibacteriaceae; Propionibacterium.

REFERENCE

1 Gabbianelli R., Battistoni A., Polio F., Carri M.T., De

AUTHORS

Mattino A., Meier B., Desideri A. and Rotilio G.

TITLE

Metal uptake of recombinant cambialistic superoxide dismutase from

JOURNAL

Propionibacterium shermanii is affected by growth conditions of

REMARK

host Escherichia coli cells

FEATURES

Location/Qualifiers

source

1.567

/organism="Propionibacterium freudenreichii"

/mol_type="genomic DNA"

/strain="P23"

/sub_species="shermanii"

/db_xref="taxon:1744"

1.567

/gene="sod"

1.567

/gene="sod"

/EC_number="1.15.1.1"

/codon_start=1

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/protein_id="CAA62838.1"

/db_xref="GI:1061202"

/db_xref="GOA:Q59673"

/db_xref="SPTREMBL:Q59673"

/translation="MAVYTLPELPDYSALEPYSGEIMELHDKKHKAAYVDCANTL
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 LDMWEHAFYTLQIKYVAGDYVKSMMNVVN"

ORIGIN

Alignment Scores:

Pred. No.: 6.2e-07 Length: 567
 Score: 91.00 Matches: 16
 Percent Similarity: 84.62% Conservative: 6
 Best Local Similarity: 61.54% Mismatches: 4
 Query Match: 62.76% Indels: 0
 DB: 1 Gaps: 0

US-09-987-190-2 (1-30) x PFSSOD (1-567)

QY 2 TyrsenleuprogluLeuaspTyrgluPheSerAlaThrGluProTyrlleSerglyGln 21

Db 10 TACACGCTGCCGGAACCTCCCTACGACTACTCGCCCTGAGCCGTACATCTCGGGTGAG 69

QY 22 TleasnGluile**Tyr 27

Db 70 ATCATGAGCTCCACCAT 87

RESULT 26

PFSSOD 567 bp DNA linear BCT 15-MAY-1998

LOCUS P.freudenreichii sod gene, partial.
DEFINITION Y09012
VERSION Y09012.1 GI:3135855
KEYWORDS cytoplasmatic protein; sod gene; superoxide dismutase.
SOURCE Propionibacterium freudenreichii
ORGANISM Propionibacterium freudenreichii
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Propionibacteriaceae; Propionibacterium.

REFERENCE 1
AUTHORS Gabbianelli, R., Battistoni, A., Polizio, F., Carri, M.T., De Martino, A., Meier, B., Desideri, A. and Rotilio, G.
TITLE Metal uptake of recombinant camilalistic superoxide dismutase from host Escherichia coli cells
JOURNAL Biochem. Biophys. Res. Commun. 216 (3), 841-847 (1995)

REFERENCE 2 (bases 1 to 567)
AUTHORS Gabbianelli, R.
TITLE Direct Submission
SUBMITTED (24-OCT-1996) R. Gabbianelli, Dept. of Biology, University Tor Vergata, Via Della Ricerca Scientifica, Rome, ITALY

FEATURES
LOCATION/Qualifiers

1..567
/organism="Propionibacterium freudenreichii"
/mol_type="genomic DNA"
/strain="p23"
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/db_xref="GOA:O59673"
/db_xref="SPRMBL:O59673"
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ORIGIN

Alignment Scores:

Pred. No.: 6.2e-07 Length: 567
Score: 91.00 Matches: 16
Percent Similarity: 84.62% Conservative: 6
Best Local Similarity: 61.54% Mismatches: 4
Query Match: 62.76% Indels: 0
DB: 1 Gaps: 0

US-09-987-190-2 (1-30) x PFSSOD (1-567)

QY 2 TyrsenleuprogluLeuaspTyrgluPheSerAlaThrGluProTyrlleSerglyGln 21

Db 70 ATCATGAGCTCCACCAT 87

RESULT 27

AE016851 302529 bp DNA linear BCT 11-AUG-2003

LOCUS Tropheryma whipplei str. Twist, section 2 of 3 of the complete genome.
DEFINITION AE016851.1 GI:28476223
VERSION AE016851.1 GI:28476223
KEYWORDS Tropheryma whipplei str. Twist
SOURCE Tropheryma whipplei str. Twist
ORGANISM Tropheryma whipplei str. Twist
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococciaceae; Cellulomonadaceae; Tropheryma.

REFERENCE 1 (bases 1 to 302529)
AUTHORS Raoult, D., Ogata, H., Audic, S., Robert, C., Sultre, K., Drancourt, M. and Claverie, J.M.
TITLE Tropheryma whipplei Twist: A Human Pathogenic Actinobacteria With a Reduced Genome
JOURNAL Genome Res. 13 (8), 1800-1809 (2003)

REFERENCE 2 (bases 1 to 302529)
AUTHORS Raoult, D., Audic, S., Robert, C., Ogata, H., Sultre, K., Drancourt, M. and Claverie, J.M.
TITLE Direct Submission
SUBMITTED (26-JUL-2002) Unite des Rickettsies, Faculte de Medecine, CNRS UMR 6020, IFR 48, Universite de la Mediterranee, 27 boulevard Jean Moulin, Marseille Cedex 05 13385, France

FEATURES
LOCATION/Qualifiers

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/mol_type="genomic DNA"
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/db_xref="GI:28476224"
/translation="MRDAASVIGMRIDRYLITEKIASGMAVYKGDILRKDVSI KIMDHVNDPKPTKEKRIAEKQIAGSNAINVAVPDGRNRILAYMMEYVPGTLR KLREKVLVYKQLEITTCYBELSSAHKGLIHRDKPENITLIGNNGQIKIGPGL FRLASNNITGTGLGTAIVSPDLIRSEADTSDVATGIMLPELITGQOPFGKQ SMVAHAKANLPMKPSANVPVSVDDIVLMGSKNPEKPSDASVLAALAKKINL ENESYTDIAEILIDFGASENLKTPQKMIKLVVLAIPVLVSQGVSVFPAQPG STVETIDTAGLTPREIKLEKGLITVTSQKYDVSQGIINLPSAGTMBEDKTL ELDLSIGRPVDDIGAGLTPSEALSLIRDRDIKIROEHSQSGGLVTSYVSKS GDLSHGGRSVSNBELVITLSSLAGAIPNIGMBEDAKALNAGLAVALIOENDVY PKGRVIRQTPSGDPTVKSALNFVSKGPDVIVPNLTGKTLHDAVDALTSLGPRVYL TTSIPLDARPAKIIITPSAGTAVKGRSVTVTPG"

ORIGIN

Alignment Scores:

Pred. No.: 6.2e-07 Length: 567
Score: 91.00 Matches: 16
Percent Similarity: 84.62% Conservative: 6
Best Local Similarity: 61.54% Mismatches: 4
Query Match: 62.76% Indels: 0
DB: 1 Gaps: 0

US-09-987-190-2 (1-30) x PFSSOD (1-567)

QY 2 TyrsenleuprogluLeuaspTyrgluPheSerAlaThrGluProTyrlleSerglyGln 21

Db 10 TACACGCTGCCGGAACCTCCCTACGACTACTCGCCCTGAGCCGTACATCTCGGGTGAG 69

QY 22 TleasnGluile**Tyr 27

Db 70 ATCATGAGCTCCACCAT 87

RESULT 27

AE016851 302529 bp DNA linear BCT 11-AUG-2003

LOCUS Tropheryma whipplei str. Twist, section 2 of 3 of the complete genome.
DEFINITION AE016851.1 GI:28476223
VERSION AE016851.1 GI:28476223
KEYWORDS Tropheryma whipplei str. Twist
SOURCE Tropheryma whipplei str. Twist
ORGANISM Tropheryma whipplei str. Twist
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococciaceae; Cellulomonadaceae; Tropheryma.

REFERENCE 1 (bases 1 to 302529)
AUTHORS Raoult, D., Ogata, H., Audic, S., Robert, C., Sultre, K., Drancourt, M. and Claverie, J.M.
TITLE Tropheryma whipplei Twist: A Human Pathogenic Actinobacteria With a Reduced Genome
JOURNAL Genome Res. 13 (8), 1800-1809 (2003)

REFERENCE 2 (bases 1 to 302529)
AUTHORS Raoult, D., Audic, S., Robert, C., Ogata, H., Sultre, K., Drancourt, M. and Claverie, J.M.
TITLE Direct Submission
SUBMITTED (26-JUL-2002) Unite des Rickettsies, Faculte de Medecine, CNRS UMR 6020, IFR 48, Universite de la Mediterranee, 27 boulevard Jean Moulin, Marseille Cedex 05 13385, France

FEATURES
LOCATION/Qualifiers

1..302529
/organism="Tropheryma whipplei str. Twist"
/mol_type="genomic DNA"
/strain="twist"
/db_xref="taxon:203267"
/complement (170..1975)
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/locus_tag="TW216"
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/db_xref="GI:28476224"
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ORIGIN

Alignment Scores:

Pred. No.: 6.2e-07 Length: 567
Score: 91.00 Matches: 16
Percent Similarity: 84.62% Conservative: 6
Best Local Similarity: 61.54% Mismatches: 4
Query Match: 62.76% Indels: 0
DB: 1 Gaps: 0

US-09-987-190-2 (1-30) x PFSSOD (1-567)

QY 2 TyrsenleuprogluLeuaspTyrgluPheSerAlaThrGluProTyrlleSerglyGln 21


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3361..4722
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3361..4722
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/EC_number="6.3.2.17"
/note="Similar to Lactobacillus casei folypolyglutamate synthase Fgs SMALL:POLC LACCA (SMALL:P15925) (428 aa) and to Corynebacterium glutamicum folypolyglutamate synthase cgl13375 SMALL:BA89768 (EMBL:AP005281) (458 aa) fasta scores: E(): 5.6e-47, 37.14% id in 455 aa"
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DPRHTGRGSLLEETIATKAGIIRKGSFVVAASQHOVQCEDEYFASINIGQSGST
ELPDKIRFEGDQCDYKVPVAGGQILDIRLGYECNEVFLPLFGYQAKNALSIAAV
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3763..3810
/gene="Fgs"
/locus_tag="TW288"
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/locus_tag="TW288"
/note="Mur ligase family, glutamate ligase domain Score = 27.3 E-value = 2.6e-05"
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4727..5056
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/locus_tag="TW289"
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/db_xref="GI:28410577"
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HNGHMQ"
4727..4906
/locus_tag="TW289"
/note="Signal peptide predicted for Unknown CDS by SignalP 2.0 HMM (Signal peptide probability 0.899) with cleavage site probability 0.318 between residues 60 and 61; signal-peptide site"
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    /locus_tag="TW290"
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    /locus_tag="TW290"
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    /db_xref="GI:28410578"
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    /note="PS00469 Nucleoside diphosphate kinases active site."
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    /locus_tag="TW290"
    /EC_number="2.7.4.6"
    /note="Similar to Streptomyces coelicolor nucleoside diphosphate kinase Ndk or SCO2612 or SCC8_23c SMALL_NDK_STRCO (SMALL:P50589) (137 aa), fasta scores: E(): 5.6e-23, 48..52% id in 136 aa, and to Dictyostelium discoideum nucleoside diphosphate kinase, cytosolic NdkB or NdkC or GtpI7 SMALL:NDKC DICTI (SMALL:P22887) (155 aa) fasta scores: E(): 3e-24, 48..5% id in 134 aa"
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    /locus_tag="TW290"
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    /EC_number="3.1.4.-"
    /note="Similar to Escherichia coli ribonuclease E Rne or Ams or Hmp1 or h1084 SMALL:RNE_ECOLI (SMALL:P21513) (1061 aa) fasta scores: E(): 9.7e-38, 36..25% id in 411 aa, and to Streptomyces coelicolor hypochelial protein SCO2599 or SCC88_10C SMALL:Q9LIH8 (EMBL:A1139298) (1340 aa) fasta scores: E(): 1.6e-58, 44..28% id in 560 aa"
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Alignment Scores:
Pred. No.:      0.0643      Length:      299050
Score:          82.00       Matches:     15
Percent Similarity: 77.78%   Conservative: 6
Best Local Similarity: 55.56% Mismatches: 6
Query Match:     56.55%   Indels:      0
Db:              1        Gaps:        0

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US-09-987-190-2 (1-30) x BK251411 (1-299050)

QY      2 TyTSeRleuProGluLeuAspTYrGluPheSeSerAlaThrGluProTYrIleSeRgIyGln 21
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QY      22 ILAaSGhIle***TYrThr 28
Db      183212 ATCATGAGCTTCATCACTCA 183192

RESULT 29
LOCUS   AB079877
DEFINITION
AB079877
Marsupenaeus japonicus sod-1 mRNA for superoxide dismutase like
protein, complete cds.
AB079877
AB079877.1 GI:18700488
Marsupenaeus japonicus
Marsupenaeus japonicus
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
Penaeidae; Marsupenaeus.
1
Soma,G., Inagawa,H., Nishizawa,T., Honda,T., Nomura,Y., Uenobe,M.,
Takahashi,Y., Itami,T. and Yokomizo,Y.
Kuruma shrimp cDNA similar to superoxide dismutase protein
published Only in database (2002)
2 (bases 1 to 655)
Soma,G., Inagawa,H., Nishizawa,T., Honda,T., Nomura,Y., Uenobe,M.,
Takahashi,Y., Itami,T. and Yokomizo,Y.
Direct Submission
Submitted (15-FEB-2002) Hiroyuki Inagawa, Tokushima Bunri
University, Institute for Health Sciences, Yamashiro-cho
Nishihama-bouji, Tokushima, Tokushima 770-8514, Japan
(E-mail:phna@okushima.bunri-u.ac.jp, Tel:81-88-622-9611 (ex.1104),
Fax:81-88-622-3217)
This study was supported by Grant-in-Aid of Recombinant Cytochrome's
Project provided by the Ministry of Agriculture, Forestry and
Fisheries, Japan (RCP2001-2230).
FEATURES
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IFWNNAPDAGRGQAIQAIDSLDSHPQGFSAAYE"

ORIGIN
Alignment Scores:
Pred. No.: 7.48e-05 Length: 655
Score: 80.00 Matches: 15
Percent Similarity: 77.78% Conservative: 6
Best local Similarity: 55.56% Mismatches: 6
Query Match: 55.17% Indels: 0
DB: 3 Gaps: 0

US-09-987-190-2 (1-30) x AB079877 (1-655)
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Db      290 CAGCTCTGCCCCCTCTCAAGTAGACGCTTAAATGCCCCCGAACACACATTCGGGATG 349

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QY 22 llaasngluile**TyrThr 28
 DB 350 ATCATGAGATCATCATCACC 370
 RESULT 30
 LOCUS AB001693
 DEFINITION Equus caballus Mn-SOD mRNA for manganese superoxide dismutase,
 complete cds.
 ACCESSION AB001693
 VERSION AB001693.1 GI:4589877
 KEYWORDS Mn-SOD; manganese superoxide dismutase.
 SOURCE Equus caballus (horse)
 ORGANISM Equus caballus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 REFERENCE
 AUTHORS Ishida,N., Katayama,Y., Sato,F., Hasegawa,T. and Mukoyama,H.
 TITLE 1 (sites)
 JOURNAL The cDNA sequences of equine antioxidative enzyme genes Cu/Zn-SOD
 MEDLINE U. Vet. Med. Sci. 61 (3), 291-294 (1999)
 PUBMED 99261591
 AUTHORS 2 (bases 1 to 954)
 REFERENCE
 TITLE Direct Submission
 AUTHORS Submitted (07-MAR-1997) Nobushige Ishida, JRA Equine Research
 JOURNAL Institute, Laboratory of Molecular and Cellular Biology; 321-4,
 Tokami-Cho, Utsunomiya, Tochigi 320-0856, Japan
 (E-mail: noishida@center.equinist.go.jp, Tel:81-28-647-0662,
 Fax:81-28-647-0686)
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 Pred. No.: 0.000119 Length: 954
 Score: 80.00 Matches: 13
 Percent Similarity: 78.57% Conservative: 9
 Best Local Similarity: 46.43% Mismatches: 6
 Query Match: 55.17% Indels: 0
 DB: 4 Gaps: 0
 US-09-987-190-2 (1-30) x AB001693 (1-954)
 QY 1 lvsTyrserlelProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 20
 DB 142 AAGCAAGGCTCCCGACCTTGACGATGATGTTATGGCGCTCTGAGCGCTCAATCAAGCC 201
 QY 21 GlnIleAsngluile**TyrThr 28
 DB 202 CAGATCATGACGTCGACACAGC 225
 CDS

RESULT 31
 LOCUS GSP312188
 DEFINITION Gordonia sp. K02 sodA gene, ORF1, ORF2 and ORF3 (partial).
 ACCESSION AJ312188
 VERSION AJ312188.1 GI:21104320
 KEYWORDS ATP-binding protein; Mn-superoxide dismutase; ORF1; ORF2; ORF3;
 sodA gene; transmembrane protein.
 SOURCE Gordonia sp. K02
 ORGANISM Gordonia sp. K02
 Bacteria; Actinobacteria; Actinomycetales; Actinomycetales;
 Corynebacterineae; Gordoniaceae; Gordonia.
 REFERENCE
 AUTHORS Berkeka,M.M.
 JOURNAL Thesis (2001) Department of Institut fuer Mikrobiologie,
 Westfaelische Wilhelms-Universitaet Muenster, Muenster, Germany
 REFERENCE
 AUTHORS Berkeka,M.M., Priefert,H. and Steinhuechel,A.
 TITLE 2
 IDENTIFICATION and characterization of an extracellular
 Mn-superoxide dismutase encoding gene (sod) of Gordonia sp. strain
 K02: A radical scavenger enzyme produced during rubber degradation
 Unpublished
 3 (bases 1 to 4439)
 REFERENCE
 AUTHORS Berkeka,M.M.
 JOURNAL Direct Submission
 Submitted (21-MAY-2001) Berkeka M.M., Institut fuer Mikrobiologie,
 Westfaelische Wilhelms-Universitaet, Corrensstrasse 3,
 48149-Muenster, D-48149, GERMANY
 FEATURES
 SOURCE
 1..4439
 Location/Qualifiers
 /organism="Gordonia sp. K02"
 /mol_type="genomic DNA"
 /strain="Kb2"
 /db_xref="taxon:160824"
 /country="Germany:Muenster"
 /note="Rubber degrading bacterium"
 1..640
 /gene="soda"
 1..3
 /gene="soda"
 11..640
 /gene="soda"
 /function="radical scavenger enzyme"
 /codon_start=1
 /evidence=experimental
 /transl_table=11
 /product="Mn-superoxide dismutase"
 /protein_id="CAC85367.1"
 /db_xref="GI:21104321"
 /db_xref="GOA:O8L1L4"
 /db_xref="SPTRMBL:O8L1L4"
 /translation="MAEYVTLADLDYDAVALEPHISGRIMELHSHKHAAYVKGANDTL
 EKLAAKRDSDITAGKVTGSLSTLSPHGHGHHNSIPFNKNSPNGGEGEGPLAAITE
 QEGGDFDKRAIFTAATTLVQSGMAVILGIDTIGKLVYILQITDGSNGIPALIIIVYML
 DMWEHAFYLDYQNVKPDVYKAMVNVVWADGGERGRKATGSGILBPA"
 complement (725..1519)
 /function="hypothetical ABC transport system"
 /note="ORF1"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"
 /protein_id="CAC85368.1"
 /db_xref="GI:21104322"
 /db_xref="GOA:O8KJR7"
 /db_xref="SPTRMBL:O8KJR7"
 /translation="YSHRSAYRLGRCCEPMKTVPLRQVPGDSFYHRLMAGTKIVTL
 ILGIMTWLPSWPAALGVAAIVITALLAGLPLGAIPEPPVWFWGLIGIVAPNASSFA
 GILGALIVRAITTLALVASSIIVITTPMADVPALAIRPLRRLPLVNEWAVA
 TALCMRGLPILIEELAVLRAARLRPLTKAGRDHSAEINGIDILITAASSALRRSAE
 MAEAITTARGTCGRITAHPARPGRSALALFVIVAVCTVAVTVTLIL"
 complement (1516..3765)
 /function="hypothetical ABC transport system"

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/note="ORF2"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="CAC85369.1"
/db_xref="GI:21104323"
/db_xref="GOA:O8KJ96"
/db_xref="SPTREMBL:O8KJ96"
/translation="MCMYPSAGSIRTAEPSCDARLHAIPTGTRGRSPAGPAADT
RHGPEVAVASGPMPEFASVALFGELTYAAVIAVIAHAGARARSTSPRPDPGPA
ARALITATVATTAFAFAMAGTGMATVLSALIGIVGDIKRGKGFALIGIATVVS
PVLGVSIVLILVLPRLITTEAMTNSLHGAKMLHGMGPDPGGMALDMSRSTIAS
HMLMIVSGTGTATSLVVAAMTIGASSPACATCPARAHIDGGRKDRVAPLPSPS
NTSLILOGARVHLDIDURIDPGRGVVANGSGKSTLAKILAGRDPSTGVNRPGL
AGLVHGSTALVLRPEIQMGSRVADVIVWGLPPGADVDEALIAEVLGSGDRET
ITLSSGQQQLAIAALARDPRLIADDEVTSVDEPGQLHLIASLPVRGLAVLI
ITHRGSEAAADRVHLEAGRVPHPPMPMPDPRDIDHRPAPDSATSLAAGPHVG
DQLAAGPHLGGPLVLDHVGVAHLPSPMEVVALTDICITVYRREGLLTYGNSGK
TTLAMIMAGLSPISGCHLSSGKFTPPAGPDGEVYTHVAGVGLGFQHARLQIQ
KVTVADEIMAGGEKVGTAEVARVIELVGLPRQMAATVVDLISGQMRRVLAGIAR
HPYMLVLEPLAQLNPMFARRSVSLPLRALADQMTIVISHDESLDSVCTRRVRLV
DGAVAADDP"
complement(1524..1526)
/note="ORF1"
/complement(3772..3773)
/note="ORF2"
/3819..3822
/note="ORF3"
/3832..>4439
/function="unknown"
/note="ORF3"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="CAC85370.1"
/db_xref="GI:21104324"
/db_xref="SPTREMBL:O8KJ95"
/translation="MSTPIELTPFQHGKINGILLISRGWESTLENTHSIVSGVRI
CRGFLPTITLIGVQRPAPASADTVGMVAISVNTDSDVEAGRLNPPALVMH
PRSRRLTCCGFGRLRLVLAAGPTLGLBHRPAGRGAEATRGELAVGIDPRVPTLV
LACSSSLGPAKPCPTGSTRSARQLGPDSCGSRCSRSLTLV"
ORIGIN

Alignment Scores:
Pred. No.: 0.000803 Length: 4439
Score: 80.00 Matches: 13
Percent Similarity: 85.71% Conservative: 11
Best Local Similarity: 46.43% Mismatches: 4
Query Match: 55.17% Indels: 0
DB: 1 Gaps: 0

US-09-987-190-2 (1-30) x GSP312188 (1-4439)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheserAlaThrGluProTyrIleSerGly 20
:::|||||:::|||||:::|||||:::|||||:::|||||
Db 17 GAATACACGCTTGCCTGCGATTCGACTACGCGGCGACTGAGCGGCACATCTCGGCG 76
QY 21 GlnIleasnGluIle**TyrThr 28
:::|||||:::|||||:::|||||
Db 77 AGGATCATGAGGCTCCACACACAGC 100

RESULT 32
E15569 812 bp DNA linear PAT 26-JUL-1999
LOCUS E15569
DEFINITION cDNA encoding Malassezia antigen protein MF-4.
ACCESSION E15569
VERSION E15569.1 GI:5710252
KEYWORDS JP 1998077296-A/4.
SOURCE unidentitied
ORGANISM unidentitied
REFERENCE 1 (bases 1 to 812)
AUTHORS Takesako,K., Daimon,H., Kuroda,M., Katou,I., Yasueda,H., Akiyama,K.

```

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TITLE and Yamaguchi,H.
JOURNAL RECOMBINANT MALASSEZIA ANTIGENIC PROTEIN AND ITS GENE
COMMENT Patent: JP 1998077296-A 4 24-MAR-1998;
TAKARA SHUZO CO LTD
OS Malassezia furfur
PN JP 1998077296-A/4
PD 24-MAR-1998
PF 05-SEP-1996 JP 1996257613
PI TAKESAKO KAZUTADA, DAIMON HISASHI, KURODA MASANOBU, PI KATOU
IKUNOSHIN.
PI YASUEDA HIROSHI, AKIYAMA KAZUO, YAMAGUCHI HIDEYO PC
C07K14/195,A61K39/35,C07H21/04,C07K7/08,C12N15/09,C12Q1/68, PC
G01N33/53,
PC G01N33/569;
CC strandedness: Double;
CC topology: linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FH source 1..812 /organism='Malassezia furfur' FT
FT /strain='TIMM2782', /clone='pMF4-4'
FT mat_peptide 2..673
FT FT /product='Malassezia antigen protein MF-4'.
FEATURES
source location/qualifiers
1..812 /organism="unidentitied"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.: 0.000149 Length: 812
Score: 79.00 Matches: 15
Percent Similarity: 70.37% Conservative: 4
Best Local Similarity: 55.56% Mismatches: 8
Query Match: 54.48% Indels: 0
DB: 6 Gaps: 0

US-09-987-190-2 (1-30) x E15569 (1-812)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheserAlaThrGluProTyrIleSerGly 20
|||||:::|||||:::|||||:::|||||:::|||||
Db 74 AAGTACACGCTGCGCGCTGCGCTGCGACTACGCGGCGGCGGCGGATCTCGGCG 133
QY 21 GlnIleasnGluIle**Tyr 27
:::|||||:::|||||
Db 134 GAGATCATGAGGAGGACGACTAC 154

RESULT 33
AR222758 812 bp mRNA linear PAT 26-SEP-2002
LOCUS AR222758
DEFINITION Sequence 7 from patent US 6432407.
ACCESSION AR222758
VERSION AR222758.1 GI:23330440
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 812)
AUTHORS Takesako,K., Okada,T., Yaginara,T., Kuroda,M., Onishi,Y., Kato,I.,
Akiyama,K., Yasueda,H., and Yamaguchi,H.
TITLE Antigenic protein originating in malassezia
JOURNAL Patent: US 6432407-A 7 13-AUG-2002;
FEATURES Location/Qualifiers
1..812
source /organism="unknown"
/mol_type="mRNA"
ORIGIN

Alignment Scores:

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Pred. No.: 0.000149 Length: 812
 Score: 79.00 Matches: 15
 Percent Similarity: 70.37% Conservative: 4
 Best Local Similarity: 55.56% Mismatches: 8
 Query Match: 54.48% Indels: 0
 DB: 6 Gaps: 0

US-09-987-190-2 (1-30) x AN222758 (1-812)
 QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrTleSerGly 20
 Db 74 AAGTACACGGCTGGCGCGCTGACACTACGCGCGCTCGAGCGCGCATCTCGGCG 133
 QY 21 GluIleAsnGluIle***Tyr 27
 Db 134 GAGATCATGAGACGCACTAC 154

RESULT 34
 LOCUS AY211085 429 bp mRNA linear INV 24-FEB-2003
 DEFINITION Farfantepenaeus aztecus cytosolic manganese superoxide dismutase
 mRNA, partial cds.
 ACCESSION AY211085 GI:28544137
 VERSION AY211085.1
 KEYWORDS Farfantepenaeus aztecus (brown shrimp)
 SOURCE Farfantepenaeus aztecus
 ORGANISM Farfantepenaeus aztecus (brown shrimp)
 Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 Eukaryota; Metazoa; Arthropoda; Decapoda; Dendrobranchiata; Penaeoidea;
 Penaeidae; Farfantepenaeus.
 1 (bases 1 to 429)
 Brouwer, M. and Brown-Peterson, N.
 Direct Submission
 Submitted (05-JAN-2003) Department of Coastal Sciences, Univ.
 Southern Mississippi, 703 East Beach Drive, Ocean Springs, MS
 39564, USA

FEATURES
 Source location/Qualifiers
 1..429
 /organism="Farfantepenaeus aztecus"
 /mol_type="mRNA"
 /db_xref="taxon:6690"
 <1..>429
 /note="antioxidant enzyme"
 /codon_start=1
 /product="cytosolic manganese superoxide dismutase"
 /protein_id="AA042752.1"
 /db_xref="GI:28544138"
 /translation="EKKIAEILGTEVDQIKKNQANADAEVAIREMAVYEGIVVQC
 AGVAGAGTAVSPOIAQMPAHINAEIGEEGGAHALPPLKXDENALEPHISGLIMELIHHTK
 HHGGTINMLIAATKTLVAEANVDVSNMALLPAIKFNGG"

ORIGIN
 Alignment Scores:
 Pred. No.: 0.000102 Length: 429
 Score: 78.00 Matches: 15
 Percent Similarity: 77.78% Conservative: 6
 Best Local Similarity: 55.56% Mismatches: 6
 Query Match: 53.79% Indels: 0
 DB: 3 Gaps: 0

US-09-987-190-2 (1-30) x AY211085 (1-429)
 QY 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrTleSerGly 21
 Db 223 CATGCTTGGCCACGCTCAAGTATGATTCAAGCCCTTGAACCTCACATCTCGGCTTG 282
 QY 22 IleAsnGluIle***TyrThr 28
 Db 283 ATCATGAGATCCACCACACA 303

RESULT 35
 LOCUS BX248360 349659 bp DNA linear BCT 06-NOV-2003

DEFINITION
 Corynebacterium diptheriae gravis NCTC13129, complete genome;
 segment 7/8.
 ACCESSION
 BX248360 BX248353
 VERSION
 BX248360.1 GI:38200856
 KEYWORDS
 complete genome.
 SOURCE
 Corynebacterium diptheriae
 Corynebacterium diptheriae
 Corynebacterium diptheriae
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterinae; Corynebacteriaceae; Corynebacterium.

REFERENCE
 AUTHORS
 1 (bases 1 to 349659)
 Cerdeno-Tarraga, A.M., Efstratiou, A., Dover, L.G., Holden, M.T.G.,
 Pallen, M., Bentley, S.D., Beara, G.S., Churcher, C., James, K.D., De
 Zoyza, A., Chillingworth, T., Cronin, A., Dowd, L., Felwell, T.,
 Hamlin, N., Holroyd, S., Jagsels, K., Moule, S., Quail, M.A.,
 Rabinowitsch, E., Rutherford, K., Thomson, N.R., Unwin, L.,
 Whitehead, S. and Barrall, B.G. Parkhill, J.
 The complete genome sequence and analysis of Corynebacterium
 diptheriae NCTC13129
 Nucleic Acids Res. 31 (22), 6516-6523 (2003)
 14602910

JOURNAL
 PUBMED
 2 (bases 1 to 349659)
 Cerdeno-Tarraga, A.M.
 Direct Submission
 Submitted (03-OCT-2003) Cerdeno-Tarraga A.M., submitted on behalf
 of the Pathogen Sequencing Unit, Sanger Institute, Wellcome Trust
 Genome Campus, Hinxton, Cambridge CB10 1SA E-mail:
 anct@sanger.ac.uk

FEATURES
 Source location/Qualifiers
 1..349659
 /organism="Corynebacterium diptheriae"
 /mol_type="genomic DNA"
 /strain="NCTC13129"
 /db_xref="taxon:1717"
 /note="biotype gravis"
 /complement(117..248)
 /locus_tag="DIP2033"
 /complement(117..248)
 /locus_tag="DIP2033"
 /note="Similar partially to the C-terminal region of
 Saccharopolyspora sp putative transposase SapX
 SWALL:052713 (EMBL:AF045021) (103 aa) fasta scores: E():
 1.3e-06, 58.53% id in 41 aa, and to Mycobacterium
 tuberculosis insertion element IS986 hypothetical 6.6 kDa
 protein SWALL:YIA2 MYCTU (SWALL:PI9772) (59 aa) fasta
 scores: E(): 9.5e-05, 60% id in 35 aa"
 /codon_start=1
 /transl_table=11
 /product="putative transposase"
 /protein_id="CAE50561.1"
 /db_xref="GI:38200857"
 /translation="WTSRTTPDMAENRRLEKENADINHTKILRTASAFPAADPS"
 /complement(join(245..352,468..584,586..636,643..867))
 /locus_tag="DIP2034"
 /pseudo
 /complement(join(245..352,468..584,586..636,643..867))
 /locus_tag="DIP2034"
 /note="Pseudogene. Similar partially to Corynebacterium
 diptheriae probable transposase for insertion sequence
 element SWALL:TRA_CORDI (SWALL:P35879) (343 aa) fasta
 scores: E(): 2.7e-38, 72.26% id in 137 aa, and to Yersinia
 pestis transposase SWALL:O68779 (EMBL:AF053947) (442 aa)
 fasta scores: E(): 9.3e-21, 35.29% id in 170 aa. Note:
 Also similar to DIP0045-DIP0041 and to DIP202-DIP2029,
 also pseudogenes. Presents frameshifts at residues 92 and
 131"
 /pseudo
 /codon_start=1
 /transl_table=11
 /product="putative transposase"
 /complement(730..867)
 /locus_tag="DIP2034"
 /note="ShMPfam hit to PF00872, Transposase, Mutator
 family"

misc_feature

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gene
1053. 1715
/locus_tag="DIP2036"
1053. 1715
/locus_tag="DIP2036"
/note="No significant database matches"
/codon_start=1
/transl_table=1
/product="Putative membrane protein"
/protein_id="CAE50563.1"
/db_xref="GI:38200858"
/translation="MEKRSIASVAAYASGAVAPANAVAVRHNDNMTCPISLTAEFVKLTGNRAQLTKQDAASYKKNSTPEPQJLRANIKRTEELARGLDDPKLDMKMLBENKKKLTNNEVFRDADLACIAGKYNSDDPDSKKEEGGNGSGNNPKLPNNPEMLPNPKKLPNNPEVTPAPPSNDAGIGVIPAASIAAVLGILAVALPFKISLIPQRLRLP"
misc_feature
1053. 1127
/locus_tag="DIP2036"
/note="Signal peptide predicted for DIP2036 by SignalP 2.0"
HMM (Signal peptide probability 1.000) with cleavage site probability 0.568 between residues 25 and 26;
signal-peptide site"
order(1068. 1196,1605. 1673)
/locus_tag="DIP2036"
/note="2 probable transmembrane helices predicted for DIP2036 by TMHMM2.0"
1503. 1556
/note="3x repeat NNPKLP"
2207. 3568
/locus_tag="DIP2037"
2207. 3568
/locus_tag="DIP2037"
2207. 3568
/locus_tag="DIP2037"
/note="Similar to Streptomyces coelicolor putative peptidase SCG22.20 SMALL:Q9X425 (EMBL:AL559779) (451 aa)
fasta scores: E(): 5.7e-70, 44.19% id in 448 aa, and to Mrcobacterium leprae hypothetical 46.6 kDa protein M1193 or MCB458.08 SMALL:Q9X7B4 (EMBL:AL049478) (442 aa)
scores: E(): 1.1e-52, 37.41% id in 441 aa"
/codon_start=1
/transl_table=1
/product="putative peptidase"
/protein_id="CAE50564.1"
/db_xref="GI:38200859"
/translation="MTKTAIQTVRPLVEKQREKIFKDLSEITSYNSVSTPECAEDHAACCAIVVALKEADINATELYLDGATTVIGTEKEPDGAPTVLLYCHYDVPAGDDTAACSDPPTLETRNGRYAVAGADCKGNTAMHMLALRAVKEAGGTGKIKPIVSESESGGAEELDLIKKHELEFEDTVLLINDSGQAVETPMTTLTGKARITVLTETLSESVHSFTIMGTENDPDMVWAPPAISIIIGFTSTPVDANINAVPVASARINLRVPEKMDANEVANNAIVEHLKHEVPGAHIDVTYDDANPFAKIDGPMOLFNSCIAGAGODDTYKIGSGGATLSEHLEVPRAELALFGVEDPQATIHSPNESVDPNRINDINAEALFLLSYSK"
misc_feature
2276. 3394
/locus_tag="DIP2037"
/note="HMM Pfam hit to PF01546, Peptidase family M20/M25/M40"
3581. 3796
/locus_tag="DIP2038"
3581. 3796
/locus_tag="DIP2038"
/note="Doubtful CDS. No strong consensus RBS upstream. No significant database matches"
/codon_start=1
/transl_table=1
/product="hypothetical protein"
/protein_id="CAE50565.1"
/db_xref="GI:38200860"
/translation="MFMRIVSSACLPAREEQFLYPKPAFPDQDGRGNVVKQKLLLATNPLALATNAPHLQTLRRPLHTPS"
3804. 4094
/locus_tag="DIP2039"
3804. 4094
/locus_tag="DIP2039"
/locus_tag="DIP2039"

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/!note="No significant database matches"
/codon_start=1
/transl_table=11
/product="Hypothetical protein"
/protein_id="CAE50566.1"
/db_xref="GI:38200861"
/translacion="MYPKPVFPDAPRGDVVKYOKLLIATNPRAAHRTPEHPITPR
RGRHTPEQRNLIPKPAFPDAPRGDVVKYOKLLIATNPRAAHRTPEHPITPR
4094..5254
/locus_tag="DIP2040"
/locus_tag="DIP2040"
/locus_tag="DIP2040"
/locus_tag="DIP2040"
/note="Similar to Mycobacterium leprae probable conserved
membrane protein M1504 SMALL:Q9CBX0 (EMBL:AL583922) (430
aa) fasta scores: E(): 1.8e-10, 31.8% id in 349 aa, and to
Mycobacterium tuberculosis hypothetical 47.1 kDa protein
Rv1159 or M1195 or M1C165.26 SMALL:006557 (EMBL:Z95584)
(431 aa) fasta scores: E(): 4.3e-10, 31.66% id in 360 aa"
/codon_start=1
/transl_table=11
/product="Putative membrane protein"
/protein_id="CAE50567.1"
/db_xref="GI:38200862"
/translacion="MYGKMSAPSIATMETALFAMFLVVOOSLSNRPSEFPPDLIA
IKKALVLDRGHGLDYREYHDLGFLTPFALIRKFSRMDNNITVWGSANPYA
LLAVILMFARKQLTGVGIAITAMAGMALIRKFSDFSGYQINLLMLFLVAMDFP
LHRTGIGLAIAGIKLTPAIFIVYVLIQRRMWSASAVYFAATVATGVVPAWDFW
TKIRPSSRSVGTOTNDPQOSLRAVLRLDAEQVITAILAVLVAGFEARRANPNAM
SLALGGITACLVSPFSWYHWWVPAVVAIFAMDFSHMALQLGVAAALASVAMF
SPHLLEFHFDFWDFCVSLIVFAGVAILISPIIGYTSARTASTGSGEPVSL"
4994..4180
/locus_tag="DIP2040"
/note="Signal peptide predicted for DIP2040 by SignalP 2.0
HKM (Signal peptide probability 0.942) with cleavage site
probability 0.430 between residues 29 and 30;
signal-peptide site"
order(4112). 4165.4280.. 4333.4370.. 4429.4439.. 4498.
4511.. 4570.4583. 4651.4664.. 4723.4844.. 4903.4922.. 4990
5048.. 5116.5135.. 5203)
/locus_tag="DIP2040"
/note="11 probable transmembrane helices predicted for
DIP2040 by TMHMM2.0"
complement(5197..6276)
/locus_tag="DIP2042"
complement(5197..6276)
/locus_tag="DIP2042"
/note="Similar to Mycobacterium tuberculosis hypothetical
42.3 kDa protein Rv0433 or MT0448 or M1C122G10.30
SMALL:Y433 MYCTU (SMALL:P96279) (376 aa) fasta scores:
E(): 3e-78, 53.44% id in 363 aa, and to Halobacterium sp
VNG31397c SMALL:Q9HPZ9 (EMBL:AE005058) (360 aa) fasta
scores: E(): 9.3e-27, 32.85% id in 350 aa"
/codon_start=1

Alignment Scores:
Pred. No.: 0.418 Length: 349659
Score: 78.00 Matches: 13
Percent Similarity: 77.78% Conservative: 8
Best Local Similarity: 48.15% Mismatch: 6
Query Match: 53.79% Indels: 0
DB: 1 Gaps: 0

US-09-987-190-2 (1-30) x BX248360 (1-349659)
QY 2 TySerLeuPProGluLeuAspGlyGluheSerAlaThrGluProTyrTlleSerGlyGln 11
Db 268265 TACGCCCTCTCTGAAGCTGATTAAGCAATACGACGCTCTCGAGCACACATCGCTGAG 268324
QY 22 TleAsnGluIle***TyrThr 28
Db 268325 ATCATGAGCTGCACCACTCC 268345
RESUIT 16

```

AX123311 600 bp DNA PAT 11-MAY-2001
 LOCUS AX123311
 DEFINITION Sequence 3227 from Patent EP108790.
 ACCESSION AX123311
 VERSION AX123311.1 GI:14040799
 KEYWORDS
 SOURCE Corynebacterium glutamicum
 ORGANISM Corynebacterium glutamicum
 Bacteria; Actinobacteria; Actinomycetales;
 Corynebacteriaceae; Corynebacterium.
 REFERENCE
 1 Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A., Novel polynucleotides Patent: EP 1108790-A 3227 20-JUN-2001; KYOWA HAKKO KOGYO CO., LTD. (JP)
 FEATURES
 1. 600
 Location/Qualifiers
 /organism="Corynebacterium glutamicum"
 /mol_type="unassigned DNA"
 /db_xref="taxon:1718"
 ORIGIN
 Alignment Scores:
 Pred. No.: 0.000236 Length: 600
 Score: 77.00 Matches: 13
 Percent Similarity: 74.07% Conservative: 7
 Best Local Similarity: 48.15% Mismatches: 7
 Query Match: 53.10% Indels: 0
 DB: Gaps: 0
 US-09-987-190-2 (1-30) x AX123311 (1-600)
 QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
 Db 10 TACGAATCCCGAGACGACTAGCATACGAGCGCTCGAGCCACATCGCGCTGAA 69
 QY 22 TLeAsnGluIle**TyrThr 28
 Db 70 ATCATGGAGCTTACCACTCC 90
 RESULT 37
 BD165428 600 bp DNA linear PAT 17-JAN-2003
 LOCUS BD165428
 DEFINITION Novel polynucleotide.
 ACCESSION BD165428.1 GI:27871240
 VERSION JP 2002191370-A/3227.
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 1 (bases 1 to 600)
 Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A., Novel polynucleotide Patent: JP 2002191370-A 3227 09-JUL-2002; KYOWA HAKKO KOGYO CO LTD
 OS Corynebacterium glutamicum
 PN JP 2002191370-A/3227
 PD 09-JUL-2002
 PF 15-DEC-2000 JP 2000405096
 PI SATOSHI NAKAGAWA, HIROSHI MIZOGUCHI, SEIKO ANDO, MIKIO HAYASHI, KEIKO OCHIAI,
 PI HARUHIKO YOKOI, NAOKO TATEISHI, AKIHIRO SENOH, MASATO IKEDA, AKIO OZAKI
 PI
 PC C12N15/09, C12N15/09, C07K14/34, C07K16/12, C07K16/40, C12M1/00, PC C12N1/15,
 PC C12N1/19, C12N1/21, C12N5/10, C12N9/00, C12N9/02, C12P7/40, C12P13/04, C12P13/08,
 PC C12P19/00, C12P19/34, C12P21/02, C12Q1/37, C12Q1/68, G01N33/53, PC G01N33/566,
 PC G01N33/569, G01N33/68, G01N37/00//C12P21/08, (C12N1/21, C12R1/15), PC (C12N1/21, C12R1/13), (C12N1/21, C12R1/01), (C12P13/08, C12R1/15),

PC C12N15/00,
 PC C12N5/00, C12N15/00
 CC Novel polynucleotide
 FH key
 FT source
 FT 1. 600
 Location/Qualifiers
 /organism="Corynebacterium glutamicum".
 /mol_type="genomic DNA"
 /db_xref="taxon:3264"
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 1. 600
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:3264"
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 Pred. No.: 0.000236 Length: 600
 Score: 77.00 Matches: 13
 Percent Similarity: 74.07% Conservative: 7
 Best Local Similarity: 48.15% Mismatches: 7
 Query Match: 53.10% Indels: 0
 DB: Gaps: 0
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 QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
 Db 10 TACGAATCCCGAGACGACTAGCATACGAGCGCTCGAGCCACATCGCGCTGAA 69
 QY 22 TLeAsnGluIle**TyrThr 28
 Db 70 ATCATGGAGCTTACCACTCC 90
 RESULT 38
 RABMSD 606 bp mRNA linear MAM 11-FEB-1994
 LOCUS RABMSD
 DEFINITION Oryctolagus cuniculus manganese superoxide dismutase mRNA, partial cds.
 ACCESSION L28808
 VERSION L28808.1 GI:454174
 KEYWORDS manganese superoxide dismutase.
 SOURCE Oryctolagus cuniculus (rabbit)
 ORGANISM Oryctolagus cuniculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 REFERENCE
 1 (bases 1 to 606)
 Jackson, R.M.
 JOURNAL Unpublished (1994)
 COMMENT Original source text: Oryctolagus cuniculus (strain NZ white) cDNA to mRNA.
 FEATURES
 source
 1. 606
 Location/Qualifiers
 /organism="Oryctolagus cuniculus"
 /mol_type="mRNA"
 /strain="NZ white"
 /db_xref="taxon:9986"
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 /product="manganese superoxide dismutase"
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 /db_xref="GI:454175"
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 ORIGIN
 Alignment Scores:
 Pred. No.: 0.000239 Length: 606
 Score: 77.00 Matches: 13
 Percent Similarity: 78.57% Conservative: 9
 Best Local Similarity: 46.43% Mismatches: 6
 Query Match: 53.10% Indels: 0
 DB: Gaps: 0

US-09-987-190-2 (1-30) x RABMSD (1-606)

QY 1 TysTerLeuProGluLeuAspTYrGluPheSerAlaThrGluProTYrIleSerGly 20
 Db 16 AAGCAGAGCTCCCGACCTGCGCTACGACTACGCGCTGAGCGCCGACATCAACCG 75
 QY 21 GlnIleAsnGluIle***TyrThr 28
 Db 76 CAGATCATGAGCTTCACCACTCC 99

RESULT 39

AB055218 960 bp DNA linear BCT 02-AUG-2001

LOCUS Corynebacterium glutamicum gene for superoxide dismutase, complete

DEFINITION AB055218 1 GI:15076595

VERSION AB055218.1

KEYWORDS Corynebacterium glutamicum

SOURCE Corynebacterium glutamicum

ORGANISM Corynebacterium glutamicum

REFERENCE Corynebacterium glutamicum

AUTHORS Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Hattori, M.,

TITLE Shiba, T., Sakaki, Y., Yokoi, H. and Ozaki, A.

JOURNAL SOD of Corynebacterium glutamicum ATCC 13032

REFERENCE Published only in Database (2001)

AUTHORS 2 (bases 1 to 960)

TITLE Nakagawa, S.

JOURNAL Direct Submission

REFERENCE Submitted (01-FEB-2001) Satoshi Nakagawa, Kyowa Hakko Kogyo Co.

AUTHORS Ltd., Tokyo Research Laboratories; 3-6-6, Asahi-machi, Machida,

TITLE Tokyo 194-8533, Japan (E-mail: snakagawa@kyowa.co.jp,

REFERENCE Tel: 81-42-725-2555 (ex. 2165), Fax: 81-42-726-8330)

AUTHORS Location/Qualifiers

TITLE 1..960

JOURNAL /organism="Corynebacterium glutamicum"

REFERENCE /mol_type="genomic DNA"

AUTHORS /strain="ATCC 13032"

TITLE /db_xref="taxon:1718"

JOURNAL 154..756

REFERENCE /EC_number="1.15.1.1"

AUTHORS /codon_start=1

TITLE /transl_table=11

JOURNAL /product="superoxide dismutase"

REFERENCE /protein_id="BAB62412.1"

AUTHORS /db_xref="GI:15076596"

TITLE /translation="MAVVELPELDVADLEPHIAAEIWEIHSKHATYVAGANAAL

JOURNAL EALEKAREGNTNDQIRALSKNIAPNLGGHTNHSVPKNDSENGSGEPTEGLAEALNR

REFERENCE DREGSPAKFDQHNHSALGLQSGMAVLGYDHTISGRLVIRQLTDQGNISVDITPVLML

AUTHORS DMWEHAFYIQYKXVKADYKAVWNVFENMDAARFAASK"

ORIGIN

Alignment Scores:

Pred. No.: 0.000423

Score: 77.00

Percent Similarity: 74.07%

Best Local Similarity: 48.15%

Query Match: 53.10%

DB: 1

US-09-987-190-2 (1-30) x AB055218 (1-960)

QY 2 TysTerLeuProGluLeuAspTYrGluPheSerAlaThrGluProTYrIleSerGly 21

Db 163 TAGCAACTCCGAGACTCGACTACGACTACGAGCTCTGAGCGACACATCGCGCTGAA 222

QY 22 IleAsnGluIle***TyrThr 28

Db 223 ATCATGAGCTTCACCACTCC 243

RESULT 40

AR338437

LOCUS

AR338437

1143 bp

DNA

linear

PAT 17-AUG-2003

DEFINITION Sequence 1 from patent US 6569650.

ACCESSION AR338437

VERSION AR338437.1 GI:33725209

KEYWORDS

SOURCE

ORGANISM

Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1143)

AUTHORS Merkmann, M., Guyonvarch, A. and Marx, A.

TITLE Process for the fermentative preparation of metabolic products and

JOURNAL Patent: US 6569650-A 1 27-MAY-2003;

FEATURES Location/Qualifiers

source 1..1143

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 0.000526

Score: 77.00

Percent Similarity: 74.07%

Best Local Similarity: 48.15%

Query Match: 53.10%

DB: 6

US-09-987-190-2 (1-30) x AR338437 (1-1143)

QY 2 TysTerLeuProGluLeuAspTYrGluPheSerAlaThrGluProTYrIleSerGly 21

Db 347 TAGCAACTCCGAGACTCGACTACGACTACGAGCTCTGAGCGACACATCGCGCTGAA 406

QY 22 IleAsnGluIle***TyrThr 28

Db 407 ATCATGAGCTTCACCACTCC 427

Search completed: August 31, 2004, 20:09:27

Job time : 6735 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

CM protein - nucleic search, using frame_plus_p2n model

Run on: August 31, 2004, 12:11:23 ; Search time 69 Seconds

(without alignments)
241.283 Million cell updates/sec

Title: US-09-987-190-2
Perfect score: 145
Sequence: 1 KYSLEPDEHSEATEPYISQINEXYTX 30

Scoring table:

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Ygapop 10.0	Ygapext 0.5	
Delop 6.0	Delapext 7.0	
Delop 6.0	Delext 7.0	

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=40
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	71.0	621	4	US-09-214-909-23
2	94	64.8	4403765	3	US-09-103-840A-2
3	94	64.8	4411529	3	US-09-103-840A-1
4	79	54.5	812	4	US-09-091-097-7
5	77	53.1	1143	4	US-09-373-731-1
6	74	51.0	594	3	US-09-075-019-1
7	74	51.0	600	6	5240847-8
8	74	51.0	600	6	5240847-9
9	74	51.0	600	6	5240847-16
10	74	51.0	600	6	5240847-17
11	74	51.0	681	3	US-09-075-019-6
12	74	51.0	813	2	US-08-927-230A-1

13	74	51.0	813	3	US-09-151-052-1	Sequence 1, Appli
14	74	51.0	829	4	US-09-023-655-1348	Sequence 1348, Ap
15	74	51.0	969	2	US-08-365-486A-27	Sequence 27, Appli
16	74	51.0	969	3	US-08-880-342-27	Sequence 27, Appli
17	74	51.0	976	3	US-09-126-109-1	Sequence 1, Appli
18	74	51.0	977	2	US-08-023-980B-2	Sequence 2, Appli
19	74	51.0	977	2	US-08-486-953A-2	Sequence 2, Appli
20	74	51.0	987	6	5240847-19	Patent No. 5240847
21	74	51.0	1032	6	5240847-25	Patent No. 5240847
22	74	51.0	3789	3	US-09-075-019-8	Sequence 8, Appli
23	74	49.0	721	4	US-09-262-856A-8	Sequence 8, Appli
24	70	48.3	1230025	4	US-09-198-452A-1	Sequence 1, Appli
25	67	46.2	99	6	5240847-7	Patent No. 5240847
26	67	46.2	1830121	4	US-09-557-884-1	Sequence 1, Appli
27	67	46.2	1830121	4	US-09-643-990A-1	Sequence 1, Appli
28	63	43.4	375	4	US-09-489-039A-5014	Sequence 5014, Ap
29	63	43.4	654	4	US-09-489-039A-5056	Sequence 5056, Ap
30	63	43.4	702	4	US-09-489-039A-4999	Sequence 4999, Ap
31	62	42.8	728	4	US-09-091-097-5	Sequence 5, Appli
32	58	40.0	675	4	US-09-543-681A-2482	Sequence 2482, Ap
33	58	40.0	719	3	US-09-411-578-39	Sequence 39, Appli
34	58	40.0	719	4	US-09-749-233-39	Sequence 39, Appli
35	58	40.0	726	4	US-09-540-236-1522	Sequence 1522, Ap
36	58	40.0	62909	4	US-09-596-002-32	Sequence 32, Appli
37	57	39.3	606	4	US-09-134-001C-747	Sequence 747, App
38	56	38.6	640681	4	US-09-790-988-1	Sequence 1, Appli
39	55	37.9	618	4	US-09-543-681A-284	Sequence 284, App
40	54	37.2	738	4	US-09-252-991A-7762	Sequence 7762, App
41	54	37.2	1145	4	US-08-956-171E-777	Sequence 777, App
42	54	37.2	1176	4	US-09-252-991A-7571	Sequence 7571, App
43	54	37.2	3393	4	US-08-956-171E-426	Sequence 426, App
44	53	36.6	780	1	US-08-445-909A-28	Sequence 28, Appli
45	53	36.6	1294	1	US-08-445-909A-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1
US-09-214-909-23
Sequence 23, Application US/09214909
Patent No. 6486382
GENERAL INFORMATION:
APPLICANT: GORDON-KAMM, WILLIAM
APPLICANT: PIERCE, DOROTHY A.
APPLICANT: BOWEN, BENJAMIN
APPLICANT: BRIDNEY, DENNIS
APPLICANT: ROSS, MARGIT
APPLICANT: SCHEONGE, CHRISTOPHER
APPLICANT: MILLER, MICHAEL D.
APPLICANT: SANDAHL, GARY
APPLICANT: WANG, LITUN
TITLE OF INVENTION: USE OF THE GREEN FLUORESCENT PROTEIN AS A SCREENABLE
FILE REFERENCE: 031229/0682
CURRENT APPLICATION NUMBER: US/09/214,909
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US97/07688
PRIORITY FILING DATE: 1997-05-01
PRIORITY APPLICATION NUMBER: 60/016,345
PRIORITY FILING DATE: 1996-05-01
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 621
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(621)
OTHER INFORMATION: Description of Artificial Sequence: Superoxide
OTHER INFORMATION: Dismutase coding sequence fused to GFPm
US-09-214-909-23

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Alignment Scores:
Pred. No.: 3,63e-10 Length: 621
Score: 103.00 Matches: 17
Percent Similarity: 92.86% Conservative: 9
Best Local Similarity: 60.71% Mismatches: 2
Query Match: 71.03% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-214-909-23 (1-621)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 7 GAGTACACGCTGCGGATCTCGATTCGACTACAGCGCCCTGGAACCCACATCTCCGGG 66
QY 21 GlnIleAsnGluIle**TyrThr 28
Db 67 CAGATCAGACGAGCTTCACCATCTCC 90

RESULT 2
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
Pred. No.: 0.00192 Length: 4403765
Score: 94.00 Matches: 15
Percent Similarity: 89.29% Conservative: 10
Best Local Similarity: 53.57% Mismatches: 3
Query Match: 64.83% Indels: 0
DB: 3 Gaps: 0

US-09-987-190-2 (1-30) x US-09-103-840A-2 (1-4403765)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 4312963 GAAATACACCTTGCCAGACGAGCTGAGGAGCACTGGAAACCCACATCTCCGGT 4313022
QY 21 GlnIleAsnGluIle**TyrThr 28
Db 4313023 CAGATCAGACGAGCTTCACCATCTCC 4313046

RESULT 3
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.: 0.00193 Length: 4411529
Score: 94.00 Matches: 15
Percent Similarity: 89.29% Conservative: 10
Best Local Similarity: 53.57% Mismatches: 3
Query Match: 64.83% Indels: 0
DB: 3 Gaps: 0

US-09-987-190-2 (1-30) x US-09-103-840A-1 (1-4411529)
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Db 4320707 GAAATACACCTTGCCAGACGAGCTGAGGAGCACTGGAAACCCACATCTCCGGT 4320766
QY 21 GlnIleAsnGluIle**TyrThr 28
Db 4320767 CAGATCAGACGAGCTTCACCATCTCC 4320790

RESULT 4
US-09-091-097-7
; Sequence 7, Application US/09091097
; Patent No. 6432407
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH
; APPLICANT: OKADO, TAKASHI
; APPLICANT: YAGIHARA, TOMOKO
; APPLICANT: KURODA, MASANOBU
; APPLICANT: ONISHI, YOSHIMI
; APPLICANT: KATO, IKUNOSHIN
; APPLICANT: AKIYAMA, KAZUO
; APPLICANT: YASUEDA, HIROSHI
; APPLICANT: YAMAGUCHI, HIDEYO
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/091,097
; CURRENT FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,191
; REFERENCE/DOCKET NUMBER: 1422-0346P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 812 base pairs
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/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 2..673
US-09-091-097-7

Alignment Scores:
Pred. No.: 1.62e-05 Length: 812
Score: 79.00 Matches: 15
Percent Similarity: 70.37% Conservative: 4
Best Local Similarity: 55.56% Mismatches: 8
Query Match: 54.48% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-091-097-7 (1-812)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 74 AAGTACACGCTCCGCGCGCTGCTACGACTACGCGCTCGAGCGCGGCGACTCTCGGCG 133

QY 21 GlnIleAsnGluIle**Tyr 27
Db 134 GAGATCATGAGACGACGACTAC 154

RESULT 5
US-09-373-731-1
/ Sequence 1, Application US/09373731
/ Patent No. 6569650
/ GENERAL INFORMATION:
/ APPLICANT: DEGUSSA-HULS AG
/ TITLE OF INVENTION: A PROCESS FOR THE FERMENTATIVE PREPARATION OF METABOLIC
/ TITLE OF INVENTION: PRODUCTS AND FOR THE NUCLEOTIDE SEQUENCES ENCODING FOR
/ FILE REFERENCE: MERKAM
/ CURRENT APPLICATION NUMBER: US/09/373, 731
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 1143
/ TYPE: DNA
/ ORGANISM: Corynebacterium melassecola
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (338) ..(937)
US-09-373-731-1

Alignment Scores:
Pred. No.: 5.99e-05 Length: 1143
Score: 77.00 Matches: 13
Percent Similarity: 74.07% Conservative: 7
Best Local Similarity: 48.15% Mismatches: 7
Query Match: 53.10% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-373-731-1 (1-1143)

QY 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 21
Db 347 TACGAACTCCGAGAACTCGACTACGACTACGAGCGCTCTCGAGCCACACATCGCGCTGAA 406

QY 22 IleAsnGluIle**TyrThr 28
Db 407 ATCATGAGCTTCACCACTCC 427

RESULT 6
US-09-075-019-1
/ Sequence 1, Application US/09075019
/ Patent No. 6130658
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```
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/ GENERAL INFORMATION:
/ APPLICANT: UTC IR459
/ TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
/ TITLE OF INVENTION: SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sheridan Rosa P.C.
/ STREET: 1700 Lincoln St., Suite 3500
/ CITY: Denver
/ STATE: CO
/ COUNTRY: USA
/ ZIP: 80203
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/075,019
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kovarik, Joseph E.
/ REGISTRATION NUMBER: 33,005
/ REFERENCE/DOCKET NUMBER: 2848-22
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (303) 863-9700
/ TELEFAX: (303) 863-0223
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 594 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..594
US-09-075-019-1

Alignment Scores:
Pred. No.: 9.28e-05 Length: 594
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 3 Gaps: 0

US-09-987-190-2 (1-30) x US-09-075-019-1 (1-594)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 1 AAGCAGACGCTCCCGCAGCTGCGCTACGACTACGCGGCGCTGGAACCTACATCAACGCG 60

QY 21 GlnIleAsnGluIle**TyrThr 28
Db 61 CAGATCATGACGCTGACCAACGAC 84

RESULT 7
5240847-8
/ Patent No. 5240847
/ APPLICANT: HECKL, KONRAD; SPEVAK, WALTER; OSTERMANN, ELINBORG;
/ ZOPHEL, ANDREAS; KRYSER, EDELTRAUD; MAURER-FOGY, INGRID;
/ WICHE-CONSTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
/ TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
/ (HMN-SOD)
/ NUMBER OF SEQUENCES: 34
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/167,261
/ FILING DATE: 11-MAR-1988
/ SEQ ID NO: 8
/ LENGTH: 600
5240847-8
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Alignment Scores:
Pred. No.: 9.41e-05 Length: 600
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0

US-09-987-190-2 (1-30) x 5240847-8 (1-600)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 4 AAGCACTCTTGGCAGACTTGCACATACGACTAGCGTCTAGAACACACATCAATGCT 63

QY 21 GlnIleAsnGluIle**TyrThr 28
Db 64 CAATCATGCATTCGACCACTCT 87

RESULT 8
5240847-9
; Patent No. 5240847
; APPLICANT: HECKL, KONRAD; SPEYAK, WALTER; OSTERMANN, ELINBORG;
; ZOPHEL, ANDREAS; KRYSER, EDELTRAUD; MAURER-FOGY, INGRID;
; WICHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
; TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
; (HMN-SOD)
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/167,261
; FILING DATE: 11-MAR-1988
; SEQ ID NO:9:
; LENGTH: 600

Alignment Scores:
Pred. No.: 9.41e-05 Length: 600
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0

US-09-987-190-2 (1-30) x 5240847-9 (1-600)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 4 AAGCACTCTTGGCAGACTTGCACATACGACTAGCGTCTAGAACACACATCAATGCT 63

QY 21 GlnIleAsnGluIle**TyrThr 28
Db 64 CAATCATGCATTCGACCACTCT 87

RESULT 9
5240847-16
; Patent No. 5240847
; APPLICANT: HECKL, KONRAD; SPEYAK, WALTER; OSTERMANN, ELINBORG;
; ZOPHEL, ANDREAS; KRYSER, EDELTRAUD; MAURER-FOGY, INGRID;
; WICHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
; TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
; (HMN-SOD)
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/167,261
; FILING DATE: 11-MAR-1988
; SEQ ID NO:16:
; LENGTH: 600

Alignment Scores:
Pred. No.: 9.41e-05 Length: 600
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10

Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0

US-09-987-190-2 (1-30) x 5240847-16 (1-600)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 4 AAGCACTCTTGGCAGACTTGCACATACGACTAGCGTCTAGAACACACATCAATGCT 63

QY 21 GlnIleAsnGluIle**TyrThr 28
Db 64 CAATCATGCATTCGACCACTCT 87

RESULT 10
5240847-17
; Patent No. 5240847
; APPLICANT: HECKL, KONRAD; SPEYAK, WALTER; OSTERMANN, ELINBORG;
; ZOPHEL, ANDREAS; KRYSER, EDELTRAUD; MAURER-FOGY, INGRID;
; WICHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
; TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
; (HMN-SOD)
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/167,261
; FILING DATE: 11-MAR-1988
; SEQ ID NO:17:
; LENGTH: 600

Alignment Scores:
Pred. No.: 9.41e-05 Length: 600
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0

US-09-987-190-2 (1-30) x 5240847-17 (1-600)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 4 AAGCACTCTTGGCAGACTTGCACATACGACTAGCGTCTAGAACACACATCAATGCT 63

QY 21 GlnIleAsnGluIle**TyrThr 28
Db 64 CAATCATGCATTCGACCACTCT 87

RESULT 11
US-09-075-019-6
; Sequence 6, Application US/09075019
; Patent No. 6190658
; GENERAL INFORMATION:
; APPLICANT: UTC IR459
; TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
; SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/075,019
; FILING DATE:
; CLASSIFICATION:

TELEFAX: (617) 442-4214
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:

```

; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
;

```

```

/      LENGTH: 813 base pairs
/      TYPE: nucleic acid
/      STRANDEDNESS: single
/      TOPOLOGY: linear
/      MOLECULE TYPE: cDNA
/      FEATURE:
/      NAME/KEY: CDS
/      LOCATION: 43..708
/      NAME/KEY: mat_peptide
/      LOCATION: 115..708
/      US-08-927-230A-1

Alignment Scores:
Pred. No.: 0.00014      Length: 813
Score: 74.00      Matches: 12
Percent Similarity: 78.57%      Conservative: 10
Best Local Similarity: 42.86%      Mismatches: 6
Query Match: 51.03%      Indels: 0
DB: 2      Gaps: 0

US-09-987-190-2 (1-30) x US-08-927-230A-1 (1-813)
QY      1 LysTyrSerLeuProGluIleuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db      115 AAGCAAGAGCTCCCGAGCTGCGCCACGACGACGACGACGACGACGACGACGACGACG 175
QY      21 GlnIleAsnGluIle***TyrThr 28
Db      175 CAGATCATGACGCTGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 198

RESULT 13
US-09-151-052-1
/ Sequence 1, Application US/09151052
/ Patent No. 6107070
/ GENERAL INFORMATION:
/ APPLICANT: Nick et al.
/ TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
/ NUMBER OF SEQUENCES: 11
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: LAHIVE & COCKFIELD
/ STREET: 28 State Street, Floor 24
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109-1875
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/151,052
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/927,230
/ FILING DATE: September 10, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Remillard, Jane
/ REGISTRATION NUMBER: 38,872
/ REFERENCE/DOCKET NUMBER: UPT-001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)227-7400
/ TELEFAX: (617)742-4214
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 813 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:

```

NAME/KEY: CDS
LOCATION: 43..708
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 115..708
US-09-151-052-1

Alignment Scores:
Pred. No.: 0.00014 Length: 813
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 3 Gaps: 0

US-09-987-190-2 (1-30) x US-09-151-052-1 (1-813)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 115 AAGCACAGCCTCCCGACCTGCGCTACGACTACGCGCGCTGGAACTCACAACGCG 174

QY 21 GlnIleAsnGluIle**TyrThr 28
DB 175 CAGATCATGCGCTGCGACACAGC 198

RESULT 14
US-09-023-655-1348
Sequence 1348, Application US/09023655
Patent No. 6607879

GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1348:
SEQUENCE CHARACTERISTICS:
LENGTH: 829 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: G34710
US-09-023-655-1348

Alignment Scores:
Pred. No.: 0.000144 Length: 829
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-023-655-1348 (1-829)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 139 AAGCACAGCCTCCCGACCTGCGCTACGACTACGCGCGCTGGAACTCACAACGCG 198

QY 21 GlnIleAsnGluIle**TyrThr 28
DB 199 CAGATCATGCGCTGCGACACAGC 222

RESULT 15
US-08-365-486A-27
Sequence 27, Application US/08365486A
Patent No. 5834306

GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0980
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 969 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: human manganese superoxide dismutase
INDIVIDUAL ISOLATE: EMBL #X59445
FEATURE:
NAME/KEY: CDS
LOCATION: 61..729
US-08-365-486A-27

Alignment Scores:
Pred. No.: 0.000176 Length: 969
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10

Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 2 Gaps: 0

US-09-987-190-2 (1-30) x US-08-365-486A-27 (1-969)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheserAlaThrGluProTyrIleSerGly 20
DB 133 AAGCAGACCTCTCCCGACCTGCTACGACTACGCGCTCGAACCCTCACATCAACCGC 192

Qy 21 GlnIleAsnGluIle**TyrThr 28
DB 193 CAGATCATGCAGCTGCACACACG 216

RESULT 16

US-08-880-342-27
Sequence 27, Application US/08880342
Patent No. 6218179

GENERAL INFORMATION:

APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 969 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: human manganese superoxide dismutase

FEATURE:
NAME/KEY: CDS
LOCATION: 61..729
US-08-880-342-27

Alignment Scores:
Pred. No.: 0.000176 Length: 969
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 3 Gaps: 0

US-09-987-190-2 (1-30) x US-08-880-342-27 (1-969)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheserAlaThrGluProTyrIleSerGly 20
DB 133 AAGCAGACCTCTCCCGACCTGCTACGACTACGCGCTCGAACCCTCACATCAACCGC 192

Qy 21 GlnIleAsnGluIle**TyrThr 28
DB 193 CAGATCATGCAGCTGCACACACG 216

RESULT 17

US-09-126-109-1
Sequence 1, Application US/09126109
Patent No. 6171856

GENERAL INFORMATION:

APPLICANT: Thijsen, Anice
APPLICANT: Holmeier, Hans-Ewald
APPLICANT: Newgard, Christopher B.
APPLICANT: Unger, Roger H.
APPLICANT: Shimabukuro, Michio
APPLICANT: Chen, Guaxun
APPLICANT: Rhodes, Christopher J.
APPLICANT: Hugl, Sigun R.
APPLICANT: Cousin, Sharon
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,109
FILING DATE: 30-JUL-1998
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,092
FILING DATE: 30-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US Unknown
FILING DATE: 03-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: McMillian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: UTSD:560
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 976 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-09-126-109-1

Alignment Scores:

Pred. No.: 0.000178 Length: 976
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 3 Gaps: 0

US-09-987-190-2 (1-30) x US-09-126-109-1 (1-976)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

Db 167 AAGCAGAGCCTCCCGACCTGCGCTACGACTACGCGCGCTGGAACCTGACATCAACCGC 226

QY 21 GlnIleAsnGluIle**TyrThr 28
Db 227 CAGATCATGCGAGCTGCACCAACGAC 250

RESULT 18

US-08-023-980B-2
Sequence 2, Application US/08023980B

Patent No. 5843641

GENERAL INFORMATION:

APPLICANT: Brown, Robert

APPLICANT: Horvitz, H. Robert

APPLICANT: Rosen, Daniel R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,

TITLE OF INVENTION: TREATMENT AND PREVENTION OF DISEASES OF CELL DEATH

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESS: Clark & Elbing LLP

STREET: 585 Commercial Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-1024

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/023,980B

FILING DATE: 26-FEB-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00786/177001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/723-4123

TELEFAX: 617/723-8962

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 977 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-023-980B-2

Alignment Scores:

Pred. No.: 0.000178 Length: 977
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 2 Gaps: 0

US-09-987-190-2 (1-30) x US-08-023-980B-2 (1-977)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

Db 168 AAGCAGAGCCTCCCGACCTGCGCTACGACTACGCGCGCTGGAACCTGACATCAACCGC 227

QY 21 GlnIleAsnGluIle**TyrThr 28
Db 228 CAGATCATGCGAGCTGCACCAACGAC 251

RESULT 19

US-08-486-953A-2
Sequence 2, Application US/08486953A

Patent No. 5849290

GENERAL INFORMATION:

APPLICANT: Brown, Robert

APPLICANT: Horvitz, H. Robert

APPLICANT: Rosen, Daniel R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,

TITLE OF INVENTION: TREATMENT AND PREVENTION OF DISEASES OF CELL DEATH

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESS: Clark & Elbing LLP

STREET: 176 Federal Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: FastSeq

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,953A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/204,052

FILING DATE: 28-FEB-1994

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00786/223002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/428-0200

TELEFAX: 617/428-7045

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 977 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-486-953A-2

Alignment Scores:

Pred. No.: 0.000178 Length: 977
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 2 Gaps: 0

US-09-987-190-2 (1-30) x US-08-486-953A-2 (1-977)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

Db 168 AAGCAGAGCCTCCCGACCTGCGCTACGACTACGCGCGCTGGAACCTGACATCAACCGC 227

QY 21 GlnIleAsnGluIle**TyrThr 28
Db 228 CAGATCATGCGAGCTGCACCAACGAC 251

RESULT 20

[illegible]

```

1 TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANSE
2 TITLE OF INVENTION: SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
3 NUMBER OF SEQUENCES: 12
4 CORRESPONDENCE ADDRESS:
5 ADDRESSEE: Sheridan Ross P.C.
6 STREET: 1700 Lincoln St., Suite 3500
7 CITY: Denver
8 STATE: CO
9 COUNTRY: USA
10 ZIP: 80203
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: Floppy disk
13 COMPUTER: IBM PC compatible
14 OPERATING SYSTEM: PC-DOS/MS-DOS
15 SOFTWARE: PatentIn Release #1.0, Version #1.30
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/09/075,019
18 FILING DATE:
19 CLASSIFICATION:
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Kovarik, Joseph E.
22 REGISTRATION NUMBER: 33,005
23 REFERENCE/DOCKET NUMBER: 2848-22
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: (303) 863-9700
26 TELEFAX: (303) 863-0223
27 INFORMATION FOR SEQ ID NO: 8:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 3789 base pairs
30 TYPE: nucleic acid
31 STRANDEDNESS: single
32 TOPOLOGY: linear
33 MOLECULE TYPE: CDNA
34 US-09-075-019-8
35
36 Alignment Scores:
37 Pred. No.: 0.00105 Length: 3789
38 Score: 74.00 Matches: 12
39 Percent Similarity: 78.57% Conservative: 10
40 Best local Similarity: 42.86% Mismatches: 6
41 Query Match: 51.03% Indels: 0
42 DB: 3 Gaps: 0
43
44 US-09-987-190-2 (1-30) x US-09-075-019-8 (1-3789)
45
46 QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
47 |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
48 Db 550 AAGACAGGCTTCCCGACCTGCGCTTACGACTACGCGCGCTTGGAACCTCACATACAGCG 605
49
50 QY 21 GlnIleAsnGluIle**TyrThr 28
51 |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
52 Db 610 CAGATCATGACGCTGCACACACAGC 633
53
54 RESULT 23
55 US-09-262-856A-8
56 Sequence 8, Application US/09262856A
57 Patent No. 633164
58 GENERAL INFORMATION:
59 APPLICANT: TAKESAKO, Kazutoh
60 APPLICANT: MIZUTANI, Shigetoshi
61 APPLICANT: ENDO, Masahiro
62 APPLICANT: KATO, Ikunoshin
63 TITLE OF INVENTION: FUNGAL ANTIGENS AND PROCESS FOR PRODUCING THE SAME
64 FILE REFERENCE: 1422-312P
65 CURRENT APPLICATION NUMBER: US/09/262,856A
66 CURRENT FILING DATE: 1999-03-04
67 NUMBER OF SEQ ID NOS: 15
68 SOFTWARE: PatentIn Ver. 2.0
69 SEQ ID NO 8
70 LENGTH: 721
71 TYPE: DNA
72 ORGANISM: Candida albicans
73 US-09-262-856A-8

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Alignment Scores:

Pred. No.:	0.000436	Length:	721
Score:	71.00	Matches:	13
Percent Similarity:	93.75%	Conservative:	2
Best Local Similarity:	81.25%	Mismatches:	1
Query Match:	48.97%	Indels:	0
DB:	4	Gaps:	0

US-09-987-190-2 (1-30) x US-09-262-856A-8 (1-721)

Qy 13 AlaThrGluProTyrIleSerGlyGlnIleAsnGluLeu***TyrThr 28

Db 1 GCCACTGACCCGTACATCACGACCAATGACCAATTCACCTACACT 48

RESULT 24

US-09-198-452A-1

Sequence 1, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: Griffiths, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 1

LENGTH: 1230025

TYPE: DNA

ORGANISM: Chlamydia pneumoniae

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)..(15000)

OTHER INFORMATION: n=a or c or g or t

NAME/KEY: misc_feature

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LOCATION: (795001)..(810000)
OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc_feature
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OTHER INFORMATION: n=a or c or g or t
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OTHER INFORMATION: n=a or c or g or t
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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (900001)..(915000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature

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Alignment Scores:

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Pred. No.: 11.4 Length: 1230025
Score: 70.00 Matches: 13
Percent Similarity: 76.19% Conservative: 3
Best Local Similarity: 61.90% Mismatches: 5
Query Match: 48.28% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-198-452A-1 (1-1230025)

QY 2 TytSerLeupProGluLeuAspTyrgluPheserAlatrhguProTyrlSerGlyln 21
Db 83327 TATTCTTACCGAGATTACCTATGATTAAGCCTTGAGCCGTATTTCTTCGAA 83386
QY 22 11e 22
Db 83387 ATT 83386

RESULT 25
5240847-7
Patent No. 5240847
APPLICANT: HECKL, KONRAD; SPEYAK, WALTER; OSTERMANN, ELINBORG;
ZOPHEL, ANDREAS; KRISTEK, EDELTRAUD; MAURER-FOGY, INGRID;
WITCHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
(HMN-SOD)
NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/167,261
FILING DATE: 11-MAR-1988
SEQ ID NO: 7:
LENGTH: 99
5240847-7

Alignment Scores:
Pred. No.: 0.000182 Length: 99
Score: 67.00 Matches: 12
Percent Similarity: 76.00% Conservative: 7
Best Local Similarity: 48.00% Mismatches: 6
Query Match: 46.21% Indels: 0
DB: 6 Gaps: 0

US-09-987-190-2 (1-30) x 5240847-7 (1-99)

QY 1 TytSerLeupProGluLeuAspTyrgluPheserAlatrhguProTyrlSerGlyln 20
Db 4 AAGCAGCTTTGCGAGCTTGCCATACGATCGATCGATGCTCTAGAACCAACATCAATGCT 63
QY 21 Gln11eAsnGlu11e 25
Db 64 CAAATCATGCAAT 78

RESULT 26
US-09-557-884-1/c
Sequence 1, Application US/09557884
Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

Alignment Scores:
Pred. No.: 69.7 Length: 1830121
Score: 67.00 Matches: 12
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 44.44% Mismatches: 9
Query Match: 46.21% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-557-884-1 (1-1830121)
QY 2 TyrsrleupProgluleuAspTyrgluPheserAlathrgluProTyrlleSerglycIn 21
Db 1152886 TACACTCTCCCTGCAATGAGCTTACCAATGCGTTAGAACCAATTGATGCGCA 1152827
QY 22 IleAsngluile***TyrlThr 28
Db 1152826 ACAATGGAATCCATCATAGT 1152806

RESULT 27
US-09-643-990A-1/c
Sequence 1, Application US/09643990A
Patent No. 6528289
GENERAL INFORMATION:
APPLICANT: Robert D. Fleischmann
Mark D. Adams
Owen White
Hamilton O. Smith
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESS: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
```

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FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
TELEFAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1

Alignment Scores:
Pred. No.: 69.7 Length: 1830121
Score: 67.00 Matches: 12
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 44.44% Mismatches: 9
Query Match: 46.21% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-643-990A-1 (1-1830121)
QY 2 TyrsrleupProgluleuAspTyrgluPheserAlathrgluProTyrlleSerglycIn 21
Db 1152886 TACACTCTCCCTGCAATGAGCTTACCAATGCGTTAGAACCAATTGATGCGCA 1152827
QY 22 IleAsngluile***TyrlThr 28
Db 1152826 ACAATGGAATCCATCATAGT 1152806

RESULT 28
US-09-489-039A-5014
Sequence 5014, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
REFERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 5014
LENGTH: 375
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5014

Alignment Scores:
Pred. No.: 0.00585 Length: 375
Score: 63.00 Matches: 12
Percent Similarity: 59.26% Conservative: 4
Best Local Similarity: 44.44% Mismatches: 11
Query Match: 43.45% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-489-039A-5014 (1-375)
QY 2 TyrsrleupProgluleuAspTyrgluPheserAlathrgluProTyrlleSerglycIn 21
Db 293 TATACCTGCGCATCCCTGCTTACGCTTAGCATGCTTGAACCGCACTTGACAAGCAG 352
QY 22 IleAsngluile***TyrlThr 28
Db 1152826 ACAATGGAATCCATCATAGT 1152806
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Db 353 ACGATGAGATCCATCACT 373

RESULT 29

US-09-489-039A-5056

/ Sequence 5056, Application US/09489039A

/ Patent No. 6610836

/ GENERAL INFORMATION:

/ APPLICANT: Gary Breton et. al

/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

/ FILE REFERENCE: 2709.2004001

/ CURRENT APPLICATION NUMBER: US/09/489,039A

/ PRIOR FILING DATE: 2000-01-27

/ PRIOR APPLICATION NUMBER: US 60/117,747

/ NUMBER OF SEQ ID NOS: 14342

/ SEQ ID NO 5056

/ LENGTH: 654

/ TYPE: DNA

/ ORGANISM: Klebsiella pneumoniae

US-09-489-039A-5056

Alignment Scores:

Pred. No.: 0.0121 Length: 654

Score: 63.00 Matches: 12

Percent Similarity: 59.26% Conservative: 4

Best Local Similarity: 44.44% Mismatches: 11

Query Match: 43.45% Indels: 0

DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-489-039A-5056 (1-654)

Qy 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21

Db 40 TATACCTGCGCATCCCTGCTTACGCTTACGATGCTCTGGAACCGCACTTGACACAGAG 99

Qy 22 IleAsnGluIle***TyrThr 28

Db 100 ACGATGAGATCCATCACT 120

RESULT 30

US-09-489-039A-4999/c

/ Sequence 4999, Application US/09489039A

/ Patent No. 6610836

/ GENERAL INFORMATION:

/ APPLICANT: Gary Breton et. al

/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

/ FILE REFERENCE: 2709.2004001

/ CURRENT APPLICATION NUMBER: US/09/489,039A

/ PRIOR FILING DATE: 2000-01-27

/ PRIOR APPLICATION NUMBER: US 60/117,747

/ NUMBER OF SEQ ID NOS: 14342

/ SEQ ID NO 4999

/ LENGTH: 702

/ TYPE: DNA

/ ORGANISM: Klebsiella pneumoniae

US-09-489-039A-4999

Alignment Scores:

Pred. No.: 0.0133 Length: 702

Score: 63.00 Matches: 12

Percent Similarity: 59.26% Conservative: 4

Best Local Similarity: 44.44% Mismatches: 11

Query Match: 43.45% Indels: 0

DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-489-039A-4999 (1-702)

Qy 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21

Db 627 TATACCTGCGCATCCCTGCTTACGCTTACGATGCTCTGGAACCGCACTTGACACAGAG 568

Qy 22 IleAsnGluIle***TyrThr 28

Db 567 ACGATGAGATCCATCACT 547

RESULT 31

US-09-091-097-5

/ Sequence 5, Application US/09091097

/ Patent No. 6432407

/ GENERAL INFORMATION:

/ APPLICANT: TAKESAKO, KAZUTOH

/ APPLICANT: OKADO, TAKASHI

/ APPLICANT: YAGIHARA, TOMOKO

/ APPLICANT: KURODA, MASANOBU

/ APPLICANT: ONISHI, YOSHIMI

/ APPLICANT: KATO, IKUNOSHIN

/ APPLICANT: AKIYAMA, KAZUO

/ APPLICANT: YASUEDA, HIROSHI

/ APPLICANT: YAMAGUCHI, HIDEYO

/ TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN

/ NUMBER OF SEQUENCES: 58

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: BIRCH, STEWART, KOIASCH & BIRCH, LLP

/ STREET: PO BOX 747

/ CITY: FALLS CHURCH

/ STATE: VA

/ COUNTRY: USA

/ ZIP: 22040-0747

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: PatentIn Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/091,097

/ FILING DATE:

/ CLASSIFICATION: 424

/ ATTORNEY/AGENT INFORMATION:

/ NAME: WEINER, MARC S.

/ REGISTRATION NUMBER: 32,181

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 703-205-8000

/ TELEFAX: 703-205-8050

/ INFORMATION FOR SEQ ID NO: 5:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 728 base pairs

/ TYPE: nucleic acid

/ STRANDEDNESS: double

/ TOPOLOGY: linear

/ MOLECULE TYPE: cDNA to mRNA

/ FEATURE:

/ NAME/KEY: CDS

/ LOCATION: 1..618

US-09-091-097-5

Alignment Scores:

Pred. No.: 0.0215 Length: 728

Score: 62.00 Matches: 11

Percent Similarity: 66.67% Conservative: 7

Best Local Similarity: 40.74% Mismatches: 9

Query Match: 42.76% Indels: 0

DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-091-097-5 (1-728)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

Db 16 GAGTACACTCTCCCTGCTTACGCTTACGATGCTCTGGAACCGCACTTGATCTTAC 75

Qy 21 GlnIleAsnGluIle***Tyr 27

Db 76 GAGATCATGACGCTGCACCAC 96

RESULT 32

US-09-543-681A-2482

; Sequence 2482, Application US/09543681A

; Patent No. 6605709

; GENERAL INFORMATION:

; APPLICANT: GARY BRETON

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

; FILE REFERENCE: 2709.1002-001

; CURRENT APPLICATION NUMBER: US/09/543.681A

; PRIOR FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/128,706

; PRIOR FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 8344

; SEQ ID NO 2482

; LENGTH: 675

; TYPE: DNA

; ORGANISM: Proteus mirabilis

US-09-543-681A-2482

Alignment Scores:

Pred. No.: 0.109 Length: 675

Score: 58.00 Matches: 11

Percent Similarity: 59.26% Conservative: 5

Best Local Similarity: 40.74% Mismatches: 11

Query Match: 40.00% Indels: 0

DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-543-681A-2482 (1-675)

QY 2 TyrsSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21

Db 58 TATACATTACCTGCACCTCCCTTATGATGCGCTAGAACCTATTGATGAGCGC 117

QY 22 IleasnGluIle***TyrThr 28

Db 118 ACATGGAAATTCACCACTACT 138

RESULT 33

US-09-411-578-39

; Sequence 39, Application US/09411578

; Patent No. 6203801

; GENERAL INFORMATION:

; APPLICANT: Schaap, Theodorus C

; APPLICANT: Kuiper, Catharina M

; APPLICANT: Vermeulen, Arnoldus N

; TITLE OF INVENTION: Coccioidosis Vaccines

; FILE REFERENCE: schaap

; CURRENT APPLICATION NUMBER: US/09/411,578

; CURRENT FILING DATE: 1999-10-04

; EARLIER APPLICATION NUMBER: 98203384.7

; EARLIER FILING DATE: 1998-10-07

; EARLIER APPLICATION NUMBER: 98203457.1

; EARLIER FILING DATE: 1998-10-16

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 39

; LENGTH: 719

; TYPE: DNA

; ORGANISM: Elimeria tenella

US-09-411-578-39

Alignment Scores:

Pred. No.: 0.119 Length: 719

Score: 58.00 Matches: 12

Percent Similarity: 53.85% Conservative: 2

Best Local Similarity: 46.15% Mismatches: 12

Query Match: 40.00% Indels: 0

DB: 3 Gaps: 0

US-09-987-190-2 (1-30) x US-09-411-578-39 (1-719)

QY 2 TyrsSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21

Db 7 TTCGAACTCCCCCGCGCTGCCGTACCATGAGCGCCCTCGAGCCGTACATCAGCAAGAG 66

QY 22 IleasnGluIle***Tyr 27

Db 67 ACTCTCGAGTACCACTAT 84

RESULT 34

US-09-749-233-39

; Sequence 39, Application US/09749233

; Patent No. 6680061

; GENERAL INFORMATION:

; APPLICANT: Schaap, Theodorus C

; APPLICANT: Kuiper, Catharina M

; APPLICANT: Vermeulen, Arnoldus N

; TITLE OF INVENTION: Coccioidosis Vaccines

; FILE REFERENCE: schaap

; CURRENT APPLICATION NUMBER: US/09/749,233

; CURRENT FILING DATE: 2000-12-27

; PRIOR FILING DATE: 1999-10-04

; PRIOR APPLICATION NUMBER: 98203457.1

; PRIOR FILING DATE: 1998-10-16

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 39

; LENGTH: 719

; TYPE: DNA

; ORGANISM: Elimeria tenella

US-09-749-233-39

Alignment Scores:

Pred. No.: 0.119 Length: 719

Score: 58.00 Matches: 12

Percent Similarity: 53.85% Conservative: 2

Best Local Similarity: 46.15% Mismatches: 12

Query Match: 40.00% Indels: 0

DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-749-233-39 (1-719)

QY 2 TyrsSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21

Db 7 TTCGAACTCCCCCGCGCTGCCGTACCATGAGCGCCCTCGAGCCGTACATCAGCAAGAG 66

QY 22 IleasnGluIle***Tyr 27

Db 67 ACTCTCGAGTACCACTAT 84

RESULT 35

US-09-540-236-1522

; Sequence 1522, Application US/09540236

; Patent No. 6673910

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS

; FILE REFERENCE: 2709.2005-001

; CURRENT APPLICATION NUMBER: US/09/540,236

; CURRENT FILING DATE: 2000-04-04

; NUMBER OF SEQ ID NOS: 3840

; SEQ ID NO 1522

; LENGTH: 726

; TYPE: DNA

; ORGANISM: M.catarrhalis

US-09-540-236-1522

Alignment Scores:

Pred. No.: 0.12 Length: 726

Score: 58.00 Matches: 10

Percent Similarity: 62.96% Conservative: 7

Job time : 1833 secs

/ TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 2709.1002-001
/ CURRENT APPLICATION NUMBER: US/09/543,681A
/ CURRENT FILING DATE: 2000-04-05
/ PRIOR APPLICATION NUMBER: US 60/128,706
/ PRIOR FILING DATE: 1999-04-09
/ NUMBER OF SEQ ID NOS: 8344
/ SEQ ID NO 284
/ LENGTH: 618
/ TYPE: DNA
/ ORGANISM: Proteus mirabilis
US-09-543-681A-284

Alignment Scores:
Pred. No.: 0.355 Length: 618
Score: 55.00 Matches: 11
Percent Similarity: 57.69% Conservative: 4
Best Local Similarity: 42.31% Mismatches: 11
Query Match: 37.93% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-543-681A-284 (1-618)

QY 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 46 TTCGAATTACCAAAATACCTTAGCGTTGATGCTCTTGAGCCACATATCTTAAGAA 105

QY 22 IleAsnGluIle**Tyr 27
Db 106 ACATTGAAATACCACTAC 123

RESULT 40

US-09-252-991A-7762
/ Sequence 7762, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ CURRENT FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 7762
/ LENGTH: 738
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7762

Alignment Scores:
Pred. No.: 0.689 Length: 738
Score: 54.00 Matches: 11
Percent Similarity: 65.22% Conservative: 4
Best Local Similarity: 47.83% Mismatches: 8
Query Match: 37.24% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-252-991A-7762 (1-738)

QY 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 163 TTCGAATTGCGCGCTGCTTACGAAAGAGCGCCCTTGAGCGCACATTTCGCGAGAA 222

QY 22 IleAsnGlu 24
Db 223 ACCCTGGAA 231

Search completed: August 31, 2004, 22:27:54

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 31, 2004, 07:14:02 ; Search time 381 Seconds

(without alignments)
334.504 Million cell updates/sec

Title: US-09-987-190-2

Perfect score: 145

Sequence: 1 KYSUPELDYEFSEATPYISQGINEIXYTX 30

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 337863 segs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2.1/USPTO.spool/US09987190/runat 24082004.161318.24720/app query.fasta_1.139
-DB=N-Geneseg.29Jan04 -QPMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPEC=0
-LOOPEXT=0 -UNIT3-bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=Pct -THR MAX=100 -THR MIN=0 -ALIGN=40
-MODE=LOCAL -OUTFMT=ptco -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09987190.@CGN 1.1.470 @runat 24082004.161318.24720 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEOUTERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N-Geneseg.29Jan04:*
1: genesegq1980s:*
2: genesegq1990s:*
3: genesegq2000s:*
4: genesegq2001as:*
5: genesegq2001bs:*
6: genesegq2002s:*
7: genesegq2003as:*
8: genesegq2003bs:*
9: genesegq2003cs:*
10: genesegq2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	69.7	900	6	ABT12955
2	94	64.8	1321	6	ABT12954
3	94	64.8	103765	4	AAI199683_43
4	94	64.8	110000	4	AAI199682_43
5	81	55.9	631	3	AAF07909
6	79	54.5	812	2	AAT95877
7	77	53.1	600	5	AAH68192
8	77	53.1	1143	4	AA500520

9	77	53.1	309400	5	AAH68534
10	74	51.0	97	2	AAQ94270
11	74	51.0	224	4	ABX40730
12	74	51.0	259	7	ABX37856
13	74	51.0	270	7	ABT33645
14	74	51.0	325	6	ABD39690
15	74	51.0	414	3	AAQ02178
16	74	51.0	424	7	ABX49579
17	74	51.0	552	2	AAZ08755
18	74	51.0	561	2	AAQ73584
19	74	51.0	561	2	AAQ73582
20	74	51.0	561	2	AAQ73585
21	74	51.0	594	2	AAQ73583
22	74	51.0	594	2	AAZ39779
23	74	51.0	600	1	AAH81225
24	74	51.0	600	1	AAH81218
25	74	51.0	600	1	AAH81224
26	74	51.0	600	1	AAH81219
27	74	51.0	600	2	AAQ94278
28	74	51.0	600	2	AAQ94271
29	74	51.0	600	2	AAQ94272
30	74	51.0	600	2	AAQ94277
31	74	51.0	609	2	AAQ20194
32	74	51.0	666	6	ABT09580
33	74	51.0	681	3	AAZ39781
34	74	51.0	813	1	AAH81370
35	74	51.0	813	1	AAH81158
36	74	51.0	813	2	AAQ53193
37	74	51.0	813	2	AAI15589
38	74	51.0	813	2	AAI15477
39	74	51.0	813	2	AAAX2498
40	74	51.0	813	2	AAA63891
41	74	51.0	849	6	ABN84891
42	74	51.0	849	6	ABA94453
43	74	51.0	897	9	ADD35245
44	74	51.0	930	9	ADE76309
45	74	51.0	966	2	AAQ94279

ALIGNMENTS

RESULT 1	
ABT12955	
ID	ABT12955 standard; DNA; 900 BP.
XX	
AC	ABT12955;
XX	
DT	29-AUG-2003 (revised)
DT	17-JAN-2003 (first entry)
XX	
DE	Mycobacterium paratuberculosis sod gene sequence.
XX	
KW	Mycobacterium paratuberculosis sod gene sequence.
XX	
OS	Mycobacterium avium subsp. paratuberculosis.
XX	
PN	W0200274991-A2.
XX	
PD	26-SEP-2002.
XX	
PF	20-MAR-2002; 2002W0-GB001308.
XX	
PR	20-MAR-2001; 2001GB-00006949.
XX	
PA	(NORC-) NORCHIP AS.
PA	(ALIA/) ALIARD S J.
XX	
PI	Karlsen F;
XX	
DR	WPI: 2002-750564/81.
DR	P-PSDB; AAO15875.
XX	
PT	Detecting the presence of Mycobacterium tuberculosis in a test sample,

Search 3

PT comprises inducing mRNA expression of Mycobacterium tuberculosis and
PT detecting the induced mRNA.
XX
PS Example 5; Page 57-58; 70pp; English.
XX
CC The invention comprises a method for detecting the presence of a micro-
CC organism (particularly Mycobacterium tuberculosis) in a test sample. The
CC method of the invention comprises exposing the test sample to an inducer
CC that is capable of inducing the expression of at least one gene in the
CC micro-organism and then testing for the presence of mRNA from this gene.
CC The method of the invention is useful for detecting an mRNA that is
CC expressed in a species of Mycobacterium (e.g. Mycobacterium
CC tuberculosis). The present DNA sequence represents a Mycobacterium gene
CC standardise OS field)
CC
SQ Sequence 900 BP; 173 A; 297 C; 277 G; 153 T; 0 U; 0 Other;
DB:
Alignment Scores:
Pred. No.: 1.89e-08 Length: 900
Score: 101.00 Matches: 17
Percent Similarity: 92.86% Conservative: 9
Best Local Similarity: 60.71% Mismatches: 2
Query Match: 69.66% Indels: 0
Gaps: 0
US-09-987-190-2 (1-30) x ABT12955 (1-900)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSeryl 20
DB 266 GAATACACCTTGGCCGACCTGGACTGAGACTGAGCGTGGAAACCGCACATCTCGGG 325
QY 21 GlnIleAsnGluIle***TyrThr 28
DB 326 CAGATCAACGAGATCCACACACC 349
RESULT 2
ABT12954
ID ABT12954 standard; DNA; 1321 BP.
XX
AC ABT12954;
XX
DT 17-JAN-2003 (first entry)
XX
DE Mycobacterium tuberculosis soda gene sequence.
XX
KM Mycobacterium detection method; gene; ds; soda; scd; prca.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200274991-A2.
XX
PD 26-SEP-2002.
XX
PF 20-MAR-2002; 2002WO-GB001308.
XX
PR 20-MAR-2001; 2001GB-00006949.
XX
PI (NORC-) NORCHIP AS.
XX (ALTA/) ALLARD S J.
XX
PI Karlsen F;
XX
DR WPI: 2002-750564/81.
XX P-PSDB; AA015874.
XX
PT Detecting the presence of Mycobacterium tuberculosis in a test sample,
PT comprises inducing mRNA expression of Mycobacterium tuberculosis and
PT detecting the induced mRNA.
XX
PS Example 5; Page 55-56; 70pp; English.
XX
CC The invention comprises a method for detecting the presence of a micro-

CC organism (particularly Mycobacterium tuberculosis) in a test sample. The
CC method of the invention comprises exposing the test sample to an inducer
CC that is capable of inducing the expression of at least one gene in the
CC micro-organism and then testing for the presence of mRNA from this gene.
CC The method of the invention is useful for detecting an mRNA that is
CC expressed in a species of Mycobacterium (e.g. Mycobacterium
CC tuberculosis). The present DNA sequence represents a Mycobacterium gene
CC which was used in an example of the invention
XX
SQ Sequence 1321 BP; 266 A; 429 C; 382 G; 244 T; 0 U; 0 Other;
DB:
Alignment Scores:
Pred. No.: 5.81e-07 Length: 1321
Score: 94.00 Matches: 15
Percent Similarity: 89.29% Conservative: 10
Best Local Similarity: 53.57% Mismatches: 3
Query Match: 64.83% Indels: 0
Gaps: 0
US-09-987-190-2 (1-30) x ABT12954 (1-1321)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSeryl 20
DB 548 GAATACACCTTGGCCGACCTGGACTGAGACTGAGCGTGGAAACCGCACATCTCGGGT 607
QY 21 GlnIleAsnGluIle***TyrThr 28
DB 608 CAGATCAACGAGATCCACACACC 631
RESULT 3
AA199683 43
Continuation (44 of 44) of AA199683 from base 4300001 (Mycobacterium tuberculosis strain
WP Sequence split into 44 fragments LOCUS AA199683 Accession AA199683
WP Fragment Name Begin End
WP AA199683_00 1 110000
WP AA199683_01 100001 210000
WP AA199683_02 200001 310000
WP AA199683_03 300001 410000
WP AA199683_04 400001 510000
WP AA199683_05 500001 610000
WP AA199683_06 600001 710000
WP AA199683_07 700001 810000
WP AA199683_08 800001 910000
WP AA199683_09 900001 1010000
WP AA199683_10 1000001 1110000
WP AA199683_11 1100001 1210000
WP AA199683_12 1200001 1310000
WP AA199683_13 1300001 1410000
WP AA199683_14 1400001 1510000
WP AA199683_15 1500001 1610000
WP AA199683_16 1600001 1710000
WP AA199683_17 1700001 1810000
WP AA199683_18 1800001 1910000
WP AA199683_19 1900001 2010000
WP AA199683_20 2000001 2110000
WP AA199683_21 2100001 2210000
WP AA199683_22 2200001 2310000
WP AA199683_23 2300001 2410000
WP AA199683_24 2400001 2510000
WP AA199683_25 2500001 2610000
WP AA199683_26 2600001 2710000
WP AA199683_27 2700001 2810000
WP AA199683_28 2800001 2910000
WP AA199683_29 2900001 3010000
WP AA199683_30 3000001 3110000
WP AA199683_31 3100001 3210000
WP AA199683_32 3200001 3310000
WP AA199683_33 3300001 3410000
WP AA199683_34 3400001 3510000
WP AA199683_35 3500001 3610000
WP AA199683_36 3600001 3710000
WP AA199683_37 3700001 3810000
WP AA199683_38 3800001 3910000

```
WP      AA199683_39      3900001      4010000
WP      AA199683_40      4000001      4110000
WP      AA199683_41      4100001      4210000
WP      AA199683_42      4200001      4310000
WP      AA199683_43      4300001      4403765

Alignment Scores:
Pred. No.:      0.000161      Length:      103765
Score:      94.00      Matches:      15
Percent Similarity:      89.29%      Conservative:      10
Best Local Similarity:      53.57%      Mismatches:      3
Query Match:      64.83%      Indels:      0
DB:      4      Gaps:      0

US-09-987-190-2 (1-30) x AA199683_43 (1-103765)

QY      1      LysTySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db      12963      GAATACACCTTGCCAGACTGGAGCTACGAGACGACGAAACGACATCTCGGGT 13022
QY      21      GlnIleAsnGluIle***TyrThr 28
Db      13023      CAGATCAACGAGCTTCACACACG 13046

RESULT 4
Continuation (44 of 45) of AA199682 from base 4300001 (Mycobacterium tuberculosis strain
WP Sequence split into 45 fragments LOCUS AA199682 Accession AA199682
WP      Fragment Name      Begin      End
WP      AA199682_00      1      110000
WP      AA199682_01      100001      210000
WP      AA199682_02      200001      310000
WP      AA199682_03      300001      410000
WP      AA199682_04      400001      510000
WP      AA199682_05      500001      610000
WP      AA199682_06      600001      710000
WP      AA199682_07      700001      810000
WP      AA199682_08      800001      910000
WP      AA199682_09      900001      1010000
WP      AA199682_10      1000001      1110000
WP      AA199682_11      1100001      1210000
WP      AA199682_12      1200001      1310000
WP      AA199682_13      1300001      1410000
WP      AA199682_14      1400001      1510000
WP      AA199682_15      1500001      1610000
WP      AA199682_16      1600001      1710000
WP      AA199682_17      1700001      1810000
WP      AA199682_18      1800001      1910000
WP      AA199682_19      1900001      2010000
WP      AA199682_20      2000001      2110000
WP      AA199682_21      2100001      2210000
WP      AA199682_22      2200001      2310000
WP      AA199682_23      2300001      2410000
WP      AA199682_24      2400001      2510000
WP      AA199682_25      2500001      2610000
WP      AA199682_26      2600001      2710000
WP      AA199682_27      2700001      2810000
WP      AA199682_28      2800001      2910000
WP      AA199682_29      2900001      3010000
WP      AA199682_30      3000001      3110000
WP      AA199682_31      3100001      3210000
WP      AA199682_32      3200001      3310000
WP      AA199682_33      3300001      3410000
WP      AA199682_34      3400001      3510000
WP      AA199682_35      3500001      3610000
WP      AA199682_36      3600001      3710000
WP      AA199682_37      3700001      3810000
WP      AA199682_38      3800001      3910000
WP      AA199682_39      3900001      4010000
WP      AA199682_40      4000001      4110000
WP      AA199682_41      4100001      4210000
WP      AA199682_42      4200001      4310000
WP      AA199682_43      4300001      4410000
```

```
WP      AA199682_44      4400001      4411529

Alignment Scores:
Pred. No.:      0.000174      Length:      110000
Score:      94.00      Matches:      15
Percent Similarity:      89.29%      Conservative:      10
Best Local Similarity:      53.57%      Mismatches:      3
Query Match:      64.83%      Indels:      0
DB:      4      Gaps:      0

US-09-987-190-2 (1-30) x AA199682_43 (1-110000)

QY      1      LysTySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db      20707      GAATACACCTTGCCAGACTGGAGCTACGAGACGACGAAACGACATCTCGGGT 20766
QY      21      GlnIleAsnGluIle***TyrThr 28
Db      20767      CAGATCAACGAGCTTCACACACG 20790

RESULT 5
AA199682_44
ID      AAF07909 standard; cDNA; 631 BP.
AC      AAF07909;
XX      13-MAR-2001 (first entry)
DT      13-MAR-2001 (first entry)
XX      Fusarium venenatum EST SEQ ID NO:432.
DE      Fusarium venenatum
XX      Multiple gene expression; filamentous fungal cell; EST;
XX      expressed sequence tag; Fusarium venenatum; Aspergillus niger;
XX      Aspergillus oryzae; Trichoderma reesei; identification; recombination;
XX      culture condition; environmental stress; spore morphogenesis;
XX      metabolic pathway engineering; catabolic pathway engineering; ss.
XX      Fusarium venenatum.
XX      OS
XX      FN
XX      WC200056762-A2.
XX      28-SEP-2000.
XX      PD
XX      22-MAR-2000; 2000MO-US007781.
XX      PF
XX      22-MAR-1999; 99US-00273623.
XX      PR
XX      (NOVO ) NOVO NORDISK BIOTECH INC.
XX      (NOVO ) NOVO NORDISK AS.
XX      PA
XX      Berka RM, Rey MW, Shuster JR, Kaupinen S, Clausen IG, Olsen PB;
XX      WPI; 2000-594572/56.
XX      PS
XX      Claim 86; Page 550; 3161pp; English.
XX      CC
XX      The present invention describes a method for monitoring differential
XX      expression of genes in a first filamentous fungal (FF) cell relative to
XX      expression of the same genes in one or more second filamentous fungal
XX      cells. The method uses fluorescence-labeled nucleic acids isolated from
XX      the FF cells and a substrate of expressed sequence tags (EST). The ESTs
XX      are used in the methods for monitoring differential expression of genes
XX      in a first filamentous fungal (FF) cell relative to expression of genes
XX      same genes in one or more second filamentous fungal cells. Monitoring the
XX      global expression of genes from FF cells allows the production potential
XX      of the microorganisms to be improved. New genes may be discovered,
XX      and possible functions of unknown open reading frames can be identified and
XX      gene copy number variation and stability can be monitored. The expression
XX      of genes can be used to study how FF cells adapt to changes in culture
XX      conditions, environmental stress, spore morphogenesis, recombination,
```

CC metabolic or catabolic pathway engineering. Using ESTs provides several
CC advantages over genomic or random cDNA clones including elimination of
CC redundancy as one spot on an array equals one gene or open reading frame,
CC and organisation of the microarrays based on function of the gene
CC products to facilitate analysis of the results. AAF07478 to AAF11247
CC represents ESTs from *Psidium venenatum*; AAF11248 to AAF11853 represents
CC ESTs from *Aspergillus niger*; AAF11854 to AAF14878 represents ESTs from
CC *Aspergillus oryzae*; and AAF14879 to AAF15337 represents ESTs from
CC *Trichoderma reesei*, which are all specifically claimed in the present
CC invention
XX
SQ Sequence 631 BP; 125 A; 223 C; 141 G; 134 T; 0 U; 8 Other;
XX
Alignment Scores:
Pred. No.: 5.21e-05 Length: 631
Score: 81.00 Matches: 15
Percent Similarity: 75.00% Conservative: 6
Best Local Similarity: 53.57% Mismatches: 7
Query Match: 55.86% Indels: 0
DB: Gaps: 0
US-09-987-190-2 (1-30) x AAF07909 (1-631)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 123 AAGGCCACTCTTCCCGATCTTCTTACNACTAGCGCGCTTGAGCCCTACATCTCTGGC 182
QY 21 GlnIleAsnGluIle***TyrThr 28
DB 183 CAGATCATGAGCTCCACCACTCC 206
RESULT 6
AAT85877
ID AAT85877 standard; cDNA to mRNA; 812 BP.
XX
AC AAT85877;
XX
DT 27-AUG-2003 (revised)
DT 23-FEB-1998 (first entry)
XX
DB Malassezia fungus MF-4 antigenic protein encoding cDNA.
XX
KM Malassezia; fungus; antigenic; human; IGE; immunoglobulin E; antibody;
KM allergy; antigen; ds.
XX
OS Malassezia.
XX
FH Key Location/Qualifiers
FH CDS 2..676
FT /*tag= a
FT /product= "MR-4_antigenic_protein"
XX
FN WO9721817-A1.
XX
PD 19-JUN-1997.
XX
PF 10-DEC-1996; 96WO-JP003602.
XX
PR 12-DEC-1995; 95JP-00346627.
PR 05-SEP-1996; 96JP-00257612.
PR 05-SEP-1996; 96JP-00257613.
XX
PA (TAKI) TAKARA SHUZO CO LTD.
XX
PI Takesako K, Okado T, Yagihara T, Kuroda M, Onishi Y, Kato I;
PI Akiyama K, Yasueda H, Yamaguchi H;
XX
XX WPI: 1997-332788/30.
DR P-PSDB; AAM29771.
XX
FT Antigenic proteins from the fungus *Malassezia* - bind to IGE antibodies
FT present in patients with *Malassezia* allergies, useful for diagnosis,
FT treatment and prevention of such conditions.
XX

XX
PS Claim 56; Page 77-78; 162pp; Japanese.
XX
CC The present sequence encodes a specifically claimed antigenic protein
CC isolated from the fungus *Malassezia*. The antigenic protein can bind to
CC IGE antibodies present in patients with allergic conditions. Antigenic
CC proteins, peptides and nucleic acids from the fungus *Malassezia* can be
CC used in the diagnosis, treatment and prevention of allergic conditions
CC due to *Malassezia* organisms (such as *M. furfur*, *M. sympodialis* and
CC *M. pachydermatitis*). (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 812 BP; 235 A; 245 C; 218 G; 114 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 0.000167 Length: 812
Score: 79.00 Matches: 15
Percent Similarity: 70.37% Conservative: 4
Best Local Similarity: 55.56% Mismatches: 8
Query Match: 54.48% Indels: 0
DB: Gaps: 0
US-09-987-190-2 (1-30) x AAT85877 (1-812)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 74 AAGTACAGCGTCCGCGCGCTCGTACGACTAGCGCGCTCGAGCGGCGATCTCGGGC 133
QY 21 GlnIleAsnGluIle***Tyr 27
DB 134 GAGATCATGAGAGACGACACTAC 154
RESULT 7
AAH68192
ID AAH68192 standard; DNA; 600 BP.
XX
AC AAH68192;
XX
DT 26-SEP-2001 (first entry)
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 3227.
XX
KM Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KM organic acid synthesis; ds.
XX
OS Corynebacterium glutamicum.
XX
FN EPI108790-A2.
XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000EP-00127688.
XX
PR 16-DEC-1999; 99JP-00377484.
PR 07-APR-2000; 2000JP-00159162.
PR 03-AUG-2000; 2000JP-00280988.
XX
PA (KYOWA) KYOWA HAKKO KOGYO KK.
XX
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
XX WPI: 2001-376931/40.
DR P-PSDB; AAG92973.
XX
FT Novel polynucleotides derived from *Coryneform* bacteria, for identifying
FT mutation point of a gene, measuring expression of a gene, analyzing
FT expression profile or pattern of a gene and identifying homologous gene.
XX
PS Claim 8; SEQ ID NO 3227; 246pp + Sequence Listing; English.
XX
CC The present invention provides a number of nucleotide and protein
CC sequences from the *Coryneform* bacterium *Corynebacterium glutamicum*. These
CC are useful for identifying the mutation point of a gene derived from a

CC mutant of coryneform bacterium, measuring expression amount and analysing
CC the expression profile or expression pattern of a gene derived from
CC Coryneform bacterium, and identifying a homologue of a gene derived from
CC coryneform bacterium. Coryneform bacteria are useful for producing amino
CC acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the European Patent Office
XX
SQ Sequence 600 BP; 143 A; 197 C; 146 G; 114 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.000261 Length: 600
Score: 77.00 Matches: 13
Percent Similarity: 74.07% Conservative: 7
Best Local Similarity: 48.15% Mismatches: 7
Query Match: 53.10% Indels: 0
DB: Gaps: 0
US-09-987-190-2 (1-30) x AAH68192 (1-600)
QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 10 TACGAATCCGAGACTCGACTACGACATGACGCTCTCGAGCCACATGCGCTGAA 69
QY 22 IleAsnGluIle**TyrThr 28
Db 70 ATCATGGAGCTTCACCACTCC 90
RESULT 8
AAH68520
ID AAH68520 standard; DNA; 1143 BP.
XX
AC AAH68520;
XX
DT 09-MAY-2001 (first entry)
XX
DE C. melassecola superoxide dismutase DNA.
XX
KM Superoxide dismutase; sod; coryneform microorganism; metabolite; ds;
XX vitamin; D-pantothenic acid; L-lysine; amplification; animal nutrition.
XX
OS Corynebacterium melassecola.
XX
XX Key Location/Qualifiers
FT CDS 338..940
FT /*tag= a
FT /product= "Superoxide dismutase"
XX
XX EPI077261-A2.
XX
XX 21-FEB-2001.
XX
XX 02-AUG-2000; 2000EP-00116669.
XX
XX 13-AUG-1999; 99US-00373731.
XX
XX (DEGS) DEGUSSA-HUELS AG.
XX (CNRS) CNRS CENT NAT RECH SCI.
XX
XX Merkmam M, Guyonvarch A, Marx A;
XX
XX WPI; 2001-212718/22.
XX P-PSDB; AAU00514.
XX
XX New DNA encoding superoxidase dismutase of Corynebacterium, useful for
XX producing transformants with increased production of metabolites,
XX particularly lysine.
XX
XX Claim 1; Page 13-14; 19pp; English.
XX
XX The sequence represents Corynebacterium melassecola superoxide dismutase
CC

CC (sod) DNA. Coryneform microorganisms may be transformed with a sod DNA
CC sequence and the sod gene can be amplified. Sod is then often
CC overexpressed in coryneform bacteria. Coryneforms that overexpress sod
CC are used for production of metabolites, particularly nucleotides,
CC vitamins and amino acids, especially D-pantothenic acid or, specifically,
CC L-lysine. These metabolites are useful in human or animal nutrition and
CC as pharmaceuticals. Overexpression of sod in coryneforms increases the
CC yield of particular metabolites
XX
SQ Sequence 1143 BP; 273 A; 323 C; 288 G; 259 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.000598 Length: 1143
Score: 77.00 Matches: 13
Percent Similarity: 74.07% Conservative: 7
Best Local Similarity: 48.15% Mismatches: 7
Query Match: 53.10% Indels: 0
DB: Gaps: 0
US-09-987-190-2 (1-30) x AAH68520 (1-1143)
QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 347 TACGAATCCGAGACTCGACTACGACATGACGCTCTCGAGCCACATGCGCTGAA 406
QY 22 IleAsnGluIle**TyrThr 28
Db 407 ATCATGGAGCTTCACCACTCC 427
RESULT 9
AAH68534
ID AAH68534 standard; DNA; 309400 BP.
XX
AC AAH68534;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 7069.
XX
KM Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
XX organic acid synthesis; ds.
XX
XX Corynebacterium glutamicum.
XX
XX EPI108790-A2.
XX
XX 20-JUN-2001.
XX
XX 18-DEC-2000; 2000EP-00127688.
XX
XX 16-DEC-1999; 99JP-00377484.
XX 07-APR-2000; 2000JP-00159162.
XX 03-AUG-2000; 2000JP-00280988.
XX
XX (XYOW) KYOWA HAKKO KOGYO KK.
XX
XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
XX Tareishi N, Senoh A, Ikeda M, Ozaki A;
XX
XX WPI; 2001-376931/40.
XX
XX Novel polynucleotides derived from Coryneform bacteria, for identifying
XX mutation point of a gene, measuring expression of a gene, analyzing
XX expression profile or pattern of a gene and identifying homologous gene.
XX
XX Disclosure; SEQ ID NO 7069; 246pp + Sequence Listing; English.
XX
XX The present invention provides a number of nucleotide and protein
XX sequences from the Coryneform bacterium Corynebacterium glutamicum. These
XX are useful for identifying the mutation point of a gene derived from a
XX mutant of coryneform bacterium, measuring expression amount and analysing
XX the expression profile or expression pattern of a gene derived from
XX Coryneform bacterium, and identifying a homologue of a gene derived from
CC

CC Coryneform bacterium. Coryneform bacteria are useful for producing amino
CC acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the European Patent Office

XX Sequence 309400 BP; 70133 A; 86477 C; 83115 G; 69675 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.817	Length:	309400
Score:	77.00	Matches:	13
Percent Similarity:	74.07%	Conservative:	7
Best Local Similarity:	48.15%	Mismatches:	7
Query Match:	53.10%	Indels:	0
DB:	5	Gaps:	0

US-09-987-190-2 (1-30) x AAH68534 (1-309400)

OY 2 TyrsereleupProgluleuAspTyrgluPheserAlathrgluProTyrlleSerGlyGln 21

Db 126401 TACCACTCCCGAAGACTGATGACATACGACGCTCTCGAGCCACATCGCCGCTGAA 126460

OY 22 Ileasnngluile**TyrThr 28

Db 126461 ATCATGAGGCTTCACCACTCC 126481

RESULT 10

AAQ94270 ID AAQ94270 standard; cDNA; 97 BP.

XX AC AAQ94270;

DT 25-MAR-2003 (revised)

DT 24-MAY-1996 (first entry)

XX Human Mn-superoxide dismutase (Lys29) N-terminal coding sequence.

XX hMn-SOD; manganese; superoxide dismutase; tetramer; inflammation;

KW autoimmune disease; rheumatoid arthritis; neoplasm; emphysema;

KM osteoarthritis; wound healing; ds.

XX Synthetic.

XX Key location/Qualifiers

FT mat_peptide 4..97

FT /*tag= a

FT /note= "only encodes partial mature protein sequence,

FT i.e. N-terminal amino acids 1-31"

XX EPE6472-A1.

XX 11-OCT-1995.

XX 10-MAR-1988; 95EP-00107460.

XX 14-MAR-1987; 87DE-03708306.

XX 26-MAY-1987; 87DE-03717695.

XX 10-JUL-1987; 87DE-03722884.

XX 24-DEC-1987; 87DE-03744038.

XX (BOEH) BOEHRINGER INGBLHEIM INT GMBH.

XX Heckl K, Spevak W, Ostermann E, Krystek E,

XX Maier-Foogy I, Wiche-Castanon M, Stratowa C, Hauptmann R,

XX WPI; 1995-346092/45.

XX Genes encoding recombinant human manganese superoxide dismutase - for

XX treatment, prevention and diagnosis of inflammatory diseases.

XX Claim 8; Page 5; 54pp; German.

CC A human placental cDNA library was screened with a probe derived from
CC published sequences of human liver MnSOD. Two sequences were isolated
CC which encoded the majority (either amino acids 22-198 or 26-198) of
CC hMnSOD. To complete the 5'-ends of the cDNA sequences, a double-stranded
CC fragment (AAQ94270) coding for an initial Met residue followed by amino
CC acids 1-31 was synthesized using yeast preferred codons. Recombinant,
CC full-length hMn-SOD is useful for treating, preventing or diagnosing
CC inflammatory, degenerative, neoplastic and rheumatic disorders; in wound
CC healing and in autoimmune diseases. (Updated on 25-MAR-2003 to correct PF
CC field.)

XX Sequence 97 BP; 30 A; 30 C; 15 G; 22 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.76e-05	Length:	97
Score:	74.00	Matches:	12
Percent Similarity:	78.57%	Conservative:	10
Best Local Similarity:	42.86%	Mismatches:	6
Query Match:	51.03%	Indels:	0
DB:	2	Gaps:	0

US-09-987-190-2 (1-30) x AAQ94270 (1-97)

OY 1 LysTyrsereleupProgluleuAspTyrgluPheserAlathrgluProTyrlleSerGly 20

Db 4 AAGACGCTTTGCCAGACTGCGCATACGACGCTGCTAGAACACACATCATGCT 63

OY 21 GlnIleasnngluile**TyrThr 28

Db 64 CAANTCATGCATTCACCACTCT 87

RESULT 11

ABX40730 ID ABX40730 standard; cDNA; 224 BP.

XX AC ABX40730;

DT 20-FEB-2003 (first entry)

XX Bovine BSR associated with lactation/muscle/fat deposition #5895.

XX Bovine; ss; EST; expressed sequence tag; lactation; LMFD;

KW muscle deposition; fat deposition; genome mapping; gene identification;

KM gene analysis; cattle breeding.

XX Bos Taurus.

XX US2002137139-A1.

XX 26-SEP-2002.

XX 24-SEP-2001; 2001US-00960352.

XX 12-JAN-1999; 99US-0115707P.

XX 11-JAN-2000; 2000US-00480902.

XX (BYAT/) BYATT J C.

XX (MATH/) MATHALAGAN N.

XX (TAON/) TAO N.

XX (WARR/) WARREN W C.

XX Byatt JC, Mathalagan N, Tao N, Warren WC;

XX WPI; 2003-110599/10.

XX New nucleic acid associated with lactation, and muscle and fat

XX deposition, useful for genome mapping, gene identification and analysis,

XX cattle breeding, or for genetically improving cattle.

XX Claim 2; SEQ ID NO 5895; 245pp; English.

XX The invention relates to a purified nucleic acid molecule associated with

XX lactation or muscle and fat deposition (designated LMFD), derived from

CC cattle, and the LMPD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
CC appearing as ABX34836-ABX49947, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMPD nucleic
CC acid linked to a promoter and a 3' non-translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 15112 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMPD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMPD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?docID=20020137139

XX SQ Sequence 224 BP; 39 A; 83 C; 74 G; 28 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.000258 Length: 224
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: Gaps: 7

US-09-987-190-2 (1-30) x ABX40730 (1-224)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 140 AAGCAGACGCTCCCGACCTGCGTACGACTACGCGCGCCCTGAGCGCCACATCAACGCG 199
|||||

QY 21 GlnIleasnGluIle***TyrThr 28
DB 200 CAGATCATGACGTGCACACACAGC 223
|||||

RESULT 12
ABX37856
ID ABX37856 standard; cDNA; 259 BP.
XX
AC ABX37856;

DT 20-FEB-2003 (first entry)

DE Bovine EST associated with lactation/muscle/fat deposition #3021.

XX Bovine; ss; EST; expressed sequence tag; lactation; LMPD;
KM muscle deposition; fat deposition; genome mapping; gene identification;
XX gene analysis; cattle breeding.

OS Bos Taurus.

XX US2002137139-A1.

PD 26-SEP-2002.

PF 24-SEP-2001; 2001US-00960352.

PR 12-JAN-1999; 99US-0115707P.

PR 11-JAN-2000; 2000US-00480302.

XX (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.

PA (WARR/) WARREN W C.

PI Byatt JC, Mathialagan N, Tao N, Warren WC;

XX WPI; 2003-110599/10.

XX New nucleic acid associated with lactation, and muscle and fat
PT deposition, useful for genome mapping, gene identification and analysis,
XX cattle breeding, or for genetically improving cattle.

PS Claim 2; SEQ ID NO 3021; 245BP; English.

XX The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMPD), derived from
CC cattle, and the LMPD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
CC appearing as ABX34836-ABX49947, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMPD nucleic
CC acid linked to a promoter and a 3' non-translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 15112 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMPD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMPD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?docID=20020137139

XX SQ Sequence 259 BP; 51 A; 96 C; 82 G; 30 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.000311 Length: 259
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: Gaps: 7

US-09-987-190-2 (1-30) x ABX37856 (1-259)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 142 AAGCAGACGCTCCCGACCTGCGTACGACTACGCGCGCCCTGAGCGCCACATCAACGCG 201
|||||

QY 21 GlnIleasnGluIle***TyrThr 28
DB 202 CAGATCATGACGTGCACACACAGC 225
|||||

RESULT 13
ABT33645
ID ABT33645 standard; DNA; 270 BP.

XX ABT33645;

DT 22-MAY-2003 (first entry)

DE Anticancer agent target gene fragment SEQ ID No 49.

XX DNA array; tumour; anticancer agent; drug tolerance factor; gene repair;
KM nucleic acid metabolism; large-scale gene-expression profiling;
XX housekeeping gene; ds.

06-OCT-2000 (first entry)
Human secreted protein 5' EST, SEQ ID NO: 2176.
Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
gene therapy; chromosome mapping; ss.
Homo sapiens.
EPI033401-A2.
06-SEP-2000.
21-FEB-2000; 2000EP-00200610.
26-FEB-1999; 99US-0122487P.
(GEST) GENSET.
Dumas Milne Edwards J, Duclert A, Giordano J,
WPI; 2000-500381/45.
P-PSDB; AAG02172.
New nucleic acid that is a 5' expressed sequence tag (5' EST) for
obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
diagnostic, forensic, gene therapy and chromosome mapping procedures.
Claim 1; SEQ ID NO 2176; 71bp + Sequence Listing; English.
The present sequence is one of a large number of 5' ESTs derived from
mRNAs encoding secreted proteins. An ORF has been identified within the
sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
derived from 30 different tissues. EST sequences usually correspond
mainly to the 3' untranslated region (UTR) of the mRNA because they are
often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
well suited for isolating cDNA sequences derived from the 5' ends of
mRNAs and even in those cases where longer cDNA sequences have been
obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
mRNAs with intact 5' ends and can therefore be used to obtain full length
cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
gene therapy and chromosome mapping procedures. They are used to obtain
upstream regulatory sequences and to design expression and secretion
vectors
SQ Sequence 414 BP; 89 A; 124 C; 126 G; 73 T; 0 U; 2 Other;
Alignment Scores:
Pred. No.: 0.000568 Length: 414
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0
US-09-987-190-2 (1-30) x AAC02178 (1-414)
1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
182 AAGCAGACGCTCCCGCAGCTGCGCTACGACACGCGCCCTCGAACCCTCACATCAACGCG 241
21 GlnIleAsnGluIle**TyrThr 28
242 CAGATCATGCGAGCTGCGACACGAGC 265
RESULT 16
ABX49579
ID ABX49579 standard; cDNA; 424 BP.
AC ABX49579;
XX
XX 21-FEB-2003 (first entry)

Bovine EST associated with lactation/muscle/fat deposition #14744.
Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
muscle deposition; fat deposition; genome mapping; gene identification;
gene analysis; cattle breeding.
Bos Taurus.
US2002137139-A1.
26-SEP-2002.
24-SEP-2001; 2001US-00960352.
12-JAN-1999; 99US-0115707P.
11-JAN-2000; 2000US-00480902.
(BYAT/) BYATT J C.
(MATH/) MATHIALAGAN N.
(TAON/) TAO N.
(WAR/) WARREN W C.
Byatt JC, Mathialagan N, Tao N, Warren WC;
WPI; 2003-110599/10.
New nucleic acid associated with lactation, and muscle and fat
deposition, useful for genome mapping, gene identification and analysis,
cattle breeding, or for genetically improving cattle.
Claim 2; SEQ ID NO 14744; 245bp; English.
The invention relates to a purified nucleic acid molecule associated with
lactation or muscle and fat deposition (designated LMFD), derived from
cattle, and the LMFD nucleic acid can specifically hybridise to a second
nucleic acid molecule comprising any of 15112 nucleotide sequences,
appearing as ABX34836-ABX49947, or complements of them. Also included are
(1) a transformed cell having a nucleic acid comprising an LMFD nucleic
acid linked to a promoter and a 3' non-translated sequence that
functions in the cell to cause termination of transcription and addition
of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
(2) determining a level or pattern of a molecule in a bovine cell or
tissue comprising: (a) incubating a marker nucleic acid (comprising any
of the 15112 nucleic acid sequences or its complement or fragment) with a
complementary nucleic acid molecule obtained from the bovine cell or
tissue, where hybridisation between the marker nucleic acid and the
complementary nucleic acid permits the detection of the molecule; and (b)
detecting the level or pattern of the complementary nucleic acid, where
the detection of the complementary nucleic acid is predictive of the
level or pattern of the molecule. The LMFD nucleic acid is used for
determining a level or pattern of a molecule in a bovine cell or tissue.
It is useful for genome mapping, gene identification and analysis; cattle
breeding; preparation of constructs for use in cattle gene expression, or
for genetically improving cattle. The present sequence is one of the
15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
present sequence was not shown in the specification but was obtained in
electronic format from the USPTO web site:
cc seqdata.uspto.gov/sequence.html?DocId=20020137139
SQ Sequence 424 BP; 95 A; 129 C; 135 G; 65 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.000586 Length: 424
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0
US-09-987-190-2 (1-30) x ABX49579 (1-424)
1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

DB 121 AAGCAGACGCTCCCGCAGCTGCGTACGACTACGCGCCCTGAGCGGCACATCAGCGC 180
QY 21 GlnIleAsnGluIle***TyrThr 28
DB 181 CAGATCATGCACTGACACACAGC 204
RESULT 17
AAZ08755
ID AAZ08755 standard; cDNA, 552 BP.
AC AAZ08755;
XX
DT 03-NOV-1999 (first entry)
XX
DE Human manganese superoxide dismutase exon 3-deleted isoform cDNA.
XX
KW Human; manganese superoxide dismutase; MnSOD; exon 3 deleted isoform;
KW MnSOD E3(-); diagnosis; viral infection; HIV; oncogenesis; tumour;
KW UV-induced damage; post ischaemia reperfusion damage; anti-inflammatory;
KW cytotoxic; cardiotoxic; cancer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key
FT 1. .552
FT CDS
FT /tag= a
FT /product= "MnSOD E3(-)"
FT /note= "manganese superoxide dismutase exon 3-deleted
FT isoform"
XX
XX W09943697-A1.
XX
XX 02-SEP-1999.
XX
XX 25-FEB-1999; 99WO-US004129.
XX
XX 25-FEB-1998; 98US-0075948P.
XX
XX (UYCO-) UNIV & COMMUNITY COLLEGE.
XX
XX Anziano PQ;
XX
XX WPI; 1999-527592/44.
XX
XX P-PSDB; AAY29656.
XX
XX A new isoform useful for diagnosing oxidative stress, and treating viral
XX infections.
XX
XX
XX PS Claim 2; Page 12; 64pp; English.
XX
XX The present sequence encodes an isoform of manganese superoxide dismutase
XX (MnSOD), which is a splice-variant lacking exon 3 of the full length
XX MnSOD (1.e. MnSOD E3(-)). MnSOD E3(-) may be useful in the treatment of a
XX wide variety of disorders including viral infections, particularly HIV,
XX and may be used for the prevention of oncogenesis, tumour promotion and
XX invasiveness, and UV-induced damage, for protection of cardiac tissue
XX against post ischaemia reperfusion damage, as an anti-inflammatory agent,
XX to reduce the cytotoxic and cardiotoxic effects of anti-cancer drugs, and
XX to improve the longevity of living cells
XX
XX Sequence 552 BP; 145 A; 135 C; 153 G; 119 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.000823 Length: 552
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 2 Gaps: 0
US-09-987-190-2 (1-30) x AAZ08755 (1-552)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 73 AAGCAGACGCTCCCGCAGCTGCGTACGACTACGCGCCCTGAGCGGCACATCAGCGC 132
QY 21 GlnIleAsnGluIle***TyrThr 28
DB 133 CAGATCATGCACTGACACACAGC 156
RESULT 18
AAQ73584
ID AAQ73584 standard; DNA, 561 BP.
AC AAQ73584;
XX
XX 25-MAR-2003 (revised)
XX
DT 25-JUN-1995 (first entry)
XX
DE Human manganese superoxide dismutase variant gene.
XX
KW MnSOD; tetramer; pulmonary oxygen toxicity; mitochondrial; mutant; ss.
XX
OS Homo sapiens.
OS
XX
XX W09421283-A1.
XX
XX 29-SEP-1994.
XX
XX 24-MAR-1994; 94WO-US003185.
XX
XX 24-MAR-1993; 93US-00036604.
XX
XX (BOEH) BOEHRINGER INGELHEIM PHARM INC.
XX
XX Megner C, Wolyniec KW;
XX
XX WPI; 1994-316659/39.
XX
XX
XX Improved inhibition of pulmonary oxygen toxicity - by propylactic,
XX topical admin. of human mitochondrial manganese superoxidisedismutase.
XX
XX
XX PS Claim 7; Page 27; 41pp; English.
XX
XX The sequence is that of a mutant human manganese superoxide dismutase
XX tetramer. Mutations of the native protein provide a protein which, when
XX applied topically, can inhibit pulmonary oxygen toxicity. See also
XX AAQ73582-5. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
XX Sequence 561 BP; 160 A; 126 C; 139 G; 136 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.000841 Length: 561
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 2 Gaps: 0
US-09-987-190-2 (1-30) x AAQ73584 (1-561)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 4 AAGCAGCTTTGGCAGACTTGCATACGACTACGCGTGTCTTGAACACACATCAATGCT 63
QY 21 GlnIleAsnGluIle***TyrThr 28
DB 64 CAAATCATGCAATTGACCACTCT 87
RESULT 19
AAQ73582
ID AAQ73582 standard; DNA, 561 BP.
XX
XX AAQ73582;
XX

DT 25-MAR-2003 (revised)
XX 25-JUN-1995 (first entry)
DE Human manganese superoxide dismutase gene.
XX MnSOD; tetramer; pulmonary oxygen toxicity; mitochondrial; mutant; ss.
OS Homo sapiens.
XX W09421283-A1.
XX 29-SEP-1994.
XX 24-MAR-1994; 94WO-US003185.
XX 24-MAR-1993; 93US-00036604.
XX (BOEH) BOEHRINGER INGELHEIM PHARM INC.
PI Wegner C, Wolynecic WW;
XX WPI; 1994-31659/39.
XX Improved inhibition of pulmonary oxygen toxicity - by propylactic,
PT topical admin. of human mitochondrial manganese superoxidisedismutase.
XX Claim 6; Page 25; 41pp; English.
XX The sequence is that of the native human manganese superoxide dismutase
CC tetramer. Mutations in this sequence, esp. CAG for AAG at codon 30 or CAT
CC for CAG at codon 32 provides a protein which, when applied topically, can
CC inhibit pulmonary oxygen toxicity. See also AAQ73583-5. (Updated on 25-
XX MAR-2003 to correct PN field.)
SQ Sequence 561 BP; 160 A; 127 C; 139 G; 135 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.000841 Length: 561
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 2 Gaps: 0
US-09-987-190-2 (1-30) x AAQ73582 (1-561)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 4 AAGCACTCTTTGCCAGACTTGCCATACGACTACGCTGCTCTAGAACACACATCAATGCT 63
QY 21 GlnIleAsnGluIle**TyrThr 28
DB 64 CAATCATGCAATGCACCACTCT 87
RESULT 20
AAQ73585
ID AAQ73585 standard; DNA; 561 BP.
XX AAQ73585;
XX 25-MAR-2003 (revised)
DT 25-JUN-1995 (first entry)
XX Human manganese superoxide dismutase variant gene.
DE MnSOD; tetramer; pulmonary oxygen toxicity; mitochondrial; mutant; ss.
XX Homo sapiens.
XX W09421283-A1.
XX 29-SEP-1994.

PF 24-MAR-1994; 94WO-US003185.
XX 24-MAR-1993; 93US-00036604.
XX (BOEH) BOEHRINGER INGELHEIM PHARM INC.
PI Wegner C, Wolynecic WW;
XX WPI; 1994-31659/39.
XX Improved inhibition of pulmonary oxygen toxicity - by propylactic,
PT topical admin. of human mitochondrial manganese superoxidisedismutase.
XX Claim 7; Page 26; 41pp; English.
XX The sequence is that of a mutant human manganese superoxide dismutase
CC tetramer. Mutations of the native protein provide a protein which, when
CC applied topically, can inhibit pulmonary oxygen toxicity. See also
CC AAQ73582-4. (Updated on 25-MAR-2003 to correct PN field.)
SQ Sequence 561 BP; 159 A; 127 C; 139 G; 136 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.000841 Length: 561
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 2 Gaps: 0
US-09-987-190-2 (1-30) x AAQ73585 (1-561)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 4 AAGCACTCTTTGCCAGACTTGCCATACGACTACGCTGCTCTAGAACACACATCAATGCT 63
QY 21 GlnIleAsnGluIle**TyrThr 28
DB 64 CAATCATGCAATGCACCACTCT 87
RESULT 21
AAQ73583
ID AAQ73583 standard; DNA; 561 BP.
XX AAQ73583;
XX 25-MAR-2003 (revised)
DT 25-JUN-1995 (first entry)
XX Human manganese superoxide dismutase variant gene.
DE MnSOD; tetramer; pulmonary oxygen toxicity; mitochondrial; mutant; ss.
XX Homo sapiens.
XX W09421283-A1.
XX 29-SEP-1994.
XX 24-MAR-1994; 94WO-US003185.
XX 24-MAR-1993; 93US-00036604.
XX (BOEH) BOEHRINGER INGELHEIM PHARM INC.
PI Wegner C, Wolynecic WW;
XX WPI; 1994-31659/39.
XX Improved inhibition of pulmonary oxygen toxicity - by propylactic,
PT topical admin. of human mitochondrial manganese superoxidisedismutase.
XX Claim 7; Page 26; 41pp; English.

CC enzymatic, biological and immunological properties of hMnSOD that are
 CC prep'd. by genetic engineering methods. Also new are DNA sequences
 CC encoding all or part of the polypeptides and replicating vectors,
 CC expression plasmids and transformed host cells contg. these sequences.
 CC hMnSOD catalyses disproportionation of the superoxide radical and can be
 CC used in the prevention, diagnosis and treatment of inflammatory,
 CC degenerative, neoplastic and rheumatoid disorders, for wound healing, in
 CC autoimmune disease and in organ transplantation. It can also be used to
 CC improve the storage stability of lfg. and solid foods. Oligo Via
 CC (XhoI/XbaI) (AAN81222) was ligated to oligo VIB (XbaI/NotI) (AAN81223)
 CC and then used to produce cDNA encoding the entire hMnSOD of formula VIIa
 CC (AAN81224) and formula VIIb. (Updated on 25-MAR-2003 to correct PR
 CC field.)
 CC
 XX SQ Sequence 600 BP; 172 A; 134 C; 150 G; 144 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0.000917 Length: 600
 Score: 74.00 Matches: 12
 Percent Similarity: 78.57% Conservative: 10
 Best Local Similarity: 42.86% Mismatches: 6
 Query Match: 51.03% Indels: 0
 Gaps: 0
 DB: 1
 US-09-987-190-2 (1-30) x AAN81225 (1-600)
 QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 Db 4 AAGCACTCTTGGCAGACTTGCATACGACTACGCTGCTCTAGAACACACATCATAGCT 63
 QY 21 GlnIleasnGluIle***TyrThr 28
 Db 64 CAATCATGCAATTGCACCACTCT 87
 RESULT 24
 AAN81218
 ID AAN81218 standard; cDNA; 600 BP.
 XX
 AC AAN81218;
 XX
 DT 25-MAR-2003 (revised)
 DT 03-OCT-1990 (first entry)
 XX
 DE Sequence of Formula IIA encoding modified portion of human manganese
 DE superoxide dismutase (hMnSOD).
 XX
 KW Human manganese superoxide dismutase derivative; clone BS8; formula IIIa;
 KW enzyme; EC-1.15.1.1.
 XX
 OS Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 4..600
 FT /*tag= a
 XX
 EP282899-A.
 PN
 XX 21-SEP-1988.
 PD
 XX 10-MAR-1988; 88BP-00103754.
 PF
 XX 14-MAR-1987; 87DE-03708306.
 PR 26-MAY-1987; 87DE-03717695.
 PR 10-JUL-1987; 87DE-03722884.
 PR 24-DEC-1987; 87DE-03744038.
 XX
 XX (BOEH) BOEHRINGER INGELHEIM.
 PA
 XX Heckl K, Spevak W, Ostermann E, Zophel A, Krystek E;
 PI Maurerfogy I, Wichnecasta MJ, Stratow C;
 XX WPI; 1988-265361/38.
 DR P-PSDB; AAP80602.

XX
 PT Prodn. of human manganese superoxide dismutase peptide(s) - and DNA coding
 PT sequences, for control and diagnosis of e.g. inflammatory diseases.
 XX
 PS Disclosure; Page 7; 57bp; German.
 XX
 CC The patent is for polypeptides, esp. non-glycosylated, having the
 CC enzymatic, biological and immunological properties of hMnSOD that are
 CC prep'd. by genetic engineering methods. Also new are DNA sequences
 CC encoding all or part of the polypeptides and replicating vectors,
 CC expression plasmids and transformed host cells contg. these sequences.
 CC hMnSOD catalyses disproportionation of the superoxide radical and can be
 CC used in the prevention, diagnosis and treatment of inflammatory,
 CC degenerative, neoplastic and rheumatoid disorders, for wound healing, in
 CC autoimmune disease and in organ transplantation. It can also be used to
 CC improve the storage stability of lfg. and solid foods. AAN81218 is
 CC derived from Formula Ia (AAN81825). (Updated on 25-MAR-2003 to correct PR
 CC field.)
 CC
 XX SQ Sequence 600 BP; 173 A; 134 C; 150 G; 143 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0.000917 Length: 600
 Score: 74.00 Matches: 12
 Percent Similarity: 78.57% Conservative: 10
 Best Local Similarity: 42.86% Mismatches: 6
 Query Match: 51.03% Indels: 0
 Gaps: 0
 DB: 1
 US-09-987-190-2 (1-30) x AAN81218 (1-600)
 QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 Db 4 AAGCACTCTTGGCAGACTTGCATACGACTACGCTGCTCTAGAACACACATCATAGCT 63
 QY 21 GlnIleasnGluIle***TyrThr 28
 Db 64 CAATCATGCAATTGCACCACTCT 87
 RESULT 25
 AAN81224
 ID AAN81224 standard; cDNA; 600 BP.
 XX
 AC AAN81224;
 XX
 DT 25-MAR-2003 (revised)
 DT 03-OCT-1990 (first entry)
 XX
 DE cDNA of formula VIIa encoding complete human manganese superoxide
 DE dismutase (hMnSOD).
 XX
 KW cDNA of formula VIIa encoding complete human manganese superoxide
 KW enzyme; EC-1.15.1.1.
 XX
 OS Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 4..600
 FT /*tag= a
 XX
 EP282899-A.
 PN
 XX 21-SEP-1988.
 PD
 XX 10-MAR-1988; 88BP-00103754.
 PF
 XX 14-MAR-1987; 87DE-03708306.
 PR 26-MAY-1987; 87DE-03717695.
 PR 10-JUL-1987; 87DE-03722884.
 PR 24-DEC-1987; 87DE-03744038.
 XX
 XX (BOEH) BOEHRINGER INGELHEIM.
 PA
 XX Heckl K, Spevak W, Ostermann E, Zophel A, Krystek E;
 PI Maurerfogy I, Wichnecasta MJ, Stratow C;
 XX WPI; 1988-265361/38.
 DR P-PSDB; AAP80602.

```
XX Prodn. of human manganese superoxidizedismutase peptide(s) - and DNA coding
PT sequences, for control and diagnosis of e.g. inflammatory diseases.
XX
XX Disclosure; Page ?; 57pp; German.
XX
CC The patent is for polypeptides, esp. non-glycosylated, having the
CC enzymatic, biological and immunological properties of hMnSOD that are
CC prep'd. by genetic engineering methods. Also new are DNA sequences
CC encoding all or part of the polypeptides and replicating vectors,
CC expression plasmids and transformed host cells contg. these sequences.
CC hMnSOD catalyses disproportionation of the superoxide radical and can be
CC used in the prevention, diagnosis and treatment of inflammatory,
CC degenerative, neoplastic and rheumatoid disorders; for wound healing; in
CC autoimmune disease and in organ transplantation. It can also be used to
CC improve the storage stability of liq. and solid foods. Oligo VIIa
CC (XhoI/XbaI) (AAN81222) was ligated to oligo VIb (XbaI/NotI) (AAN81223)
CC and then used to produce cDNA encoding the entire hMnSOD of formula VIIa
CC and formula VIIb (AAN81225). (Updated on 25-MAR-2003 to correct PR
CC field.)
XX
SQ Sequence 600 BP; 173 A; 133 C; 150 G; 144 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.000917 Length: 600
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0
US-09-987-190-2 (1-30) x AAN81224 (1-600)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 20
Db 4 AAGGACCTCTTGGCCAGACTTGCATACGACTGCGTGTCTAGAACACACATCAATGCT 63
QY 21 GlnIleAsnGluIle***TyrThr 28
Db 64 CAATCATGCATTCACACACTCT 87
RESULT 26
AAN81219
ID AAN81219 standard; cDNA; 600 BP.
XX
XX AAN81219;
XX
XX 25-MAR-2003 (revised)
DT 03-OCT-1990 (first entry)
XX
DE Sequence of Formula IIb encoding modified portion of human manganese
DE superoxide dismutase (hMnSOD).
XX
XX Human manganese superoxide dismutase derivative; clone BS8; formula IIb;
KW enzyme; EC-1.15.1.1.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 4..600
FT /*tag= a
XX
XX EP282899-A.
XX
XX 21-SEP-1988.
XX
XX 10-MAR-1988; 88EP-00103754.
XX
XX 14-MAR-1987; 87DE-03708306.
XX 26-MAY-1987; 87DE-03717695.
XX 10-JUL-1987; 87DE-03722884.
XX 24-DEC-1987; 87DE-03744038.
XX
```

```
PA (BOEH ) BOEHRINGER INGELHEIM.
XX
XX Heckl K, Spevak W, Ostermann E, Zophel A, Krystek E;
PI Maurerfogy I, Michcascata Wu, Stralow C;
XX
XX WPI; 1988-265361/38.
DR P-PSDB; AAP80603.
XX
PT Prodn. of human manganese superoxidizedismutase peptide(s) - and DNA coding
PT sequences, for control and diagnosis of e.g. inflammatory diseases.
XX
XX Disclosure; Page ?; 57pp; German.
XX
CC The patent is for polypeptides, esp. non-glycosylated, having the
CC enzymatic, biological and immunological properties of hMnSOD that are
CC prep'd. by genetic engineering methods. Also new are DNA sequences
CC encoding all or part of the polypeptides and replicating vectors,
CC expression plasmids and transformed host cells contg. these sequences.
CC hMnSOD catalyses disproportionation of the superoxide radical and can be
CC used in the prevention, diagnosis and treatment of inflammatory,
CC degenerative, neoplastic and rheumatoid disorders; for wound healing; in
CC autoimmune disease and in organ transplantation. It can also be used to
CC improve the storage stability of liq. and solid foods. AAN81219 is
CC derived from Formula I (AAN81826). (Updated on 25-MAR-2003 to correct PR
CC field.)
XX
SQ Sequence 600 BP; 172 A; 135 C; 150 G; 143 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.000917 Length: 600
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0
US-09-987-190-2 (1-30) x AAN81219 (1-600)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 20
Db 4 AAGGACCTCTTGGCCAGACTTGCATACGACTGCGTGTCTAGAACACACATCAATGCT 63
QY 21 GlnIleAsnGluIle***TyrThr 28
Db 64 CAATCATGCATTCACACACTCT 87
RESULT 27
AAQ94278
ID AAQ94278 standard; cDNA; 600 BP.
XX
XX AAQ94278;
XX
XX 25-MAR-2003 (revised)
DT 23-MAY-1996 (first entry)
XX
DE Human manganese superoxide dismutase (Gln29) coding sequence.
XX
XX hMn-SOD; manganese; superoxide dismutase; tetramer; inflammation;
KW autoimmune disease; rheumatoid arthritis; neoplasia; emphysema;
KW osteoarthritis; wound healing; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT CDS 1..600
FT /*tag= a
FT /product= "Met hMn-SOD(Gln29)"
FT /note= "the first 31 codons are provided by a synthetic
FT linker sequence"
XX
XX EP676472-A1.
XX
```


PD 11-OCT-1995.
XX
PF 10-MAR-1988; 95EP-00107460.
XX
PR 14-MAR-1987; 87DE-03708306.
PR 26-MAY-1987; 87DE-03717695.
PR 10-JUL-1987; 87DE-03722884.
PR 24-DEC-1987; 87DE-03744038.
XX
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
XX
PI Heckl K, Spevak W, Ostermann E, Zoepfel A, Krystek E,
PI Maurer-Fogy I, Wiche-Castanon M, Stratowa C, Hauptmann R;
XX WPI; 1995-346092/45.
DR
XX Genes encoding recombinant human manganese superoxide dismutase - for
PT treatment, prevention and diagnosis of inflammatory diseases.
XX
XX
PS Claim 8; Page 17-18; 54pp; German.
XX
CC The present sequence codes for a Met residue followed by the 198 amino
CC acid long hMn-SOD mature polypeptide having a Gln residue at position 29.
CC The cDNA can be inserted into expression vectors containing appropriate
CC signal sequences, etc. for expression of recombinant hMn-SOD. The N-
CC terminal Met residue can be removed, e.g. by treatment with CNBr or CNCl.
CC Mature hMn-SOD is useful for treating, preventing or diagnosing
CC inflammatory, degenerative, neoplastic and rheumatic disorders; in wound
CC healing and in autoimmune diseases. (Updated on 25-MAR-2003 to correct PF
CC field.)
XX
SQ Sequence 600 BP; 172 A; 134 C; 150 G; 144 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 0.000917 Length: 600
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0
DB: 2
US-09-987-190-2 (1-30) x AAQ94278 (1-600)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSercly 20
Db 4 AAGCACTCTTGGCAGACTTGCATACGACTACGCTGCTAGAACACACATCATGCT 63
QY 21 GlnIleAsnGluIle***TyrThr 28
Db 64 CAAATCATGCATTCACACACTCT 87
RESULT 28
AAQ94271
ID AAQ94271 standard; cDNA; 600 BP.
XX
AC AAQ94271;
XX
DT 25-MAR-2003 (revised)
DT 17-MAY-1996 (first entry)
XX
DE Human manganese superoxide dismutase (lys29) coding sequence.
XX
KM hMn-SOD; manganese; superoxide dismutase; tetramer; inflammation;
KM autoimmune disease; rheumatoid arthritis; neoplasm; emphysema;
KM osteoarthritis; wound healing; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH CDS 1..600
FT /*tag= a
FT /product= "Met_hMn-SOD (lys29)"
XX

EN E676472-A1.
XX
PD 11-OCT-1995.
XX
PF 10-MAR-1988; 95EP-00107460.
XX
PR 14-MAR-1987; 87DE-03708306.
PR 26-MAY-1987; 87DE-03717695.
PR 10-JUL-1987; 87DE-03722884.
PR 24-DEC-1987; 87DE-03744038.
XX
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
XX
PI Heckl K, Spevak W, Ostermann E, Zoepfel A, Krystek E,
PI Maurer-Fogy I, Wiche-Castanon M, Stratowa C, Hauptmann R;
XX WPI; 1995-346092/45.
DR
XX P-PSDB; AAR75191.
DR
XX Genes encoding recombinant human manganese superoxide dismutase - for
PT treatment, prevention and diagnosis of inflammatory diseases.
XX
XX
PS Claim 8; Page 6; 54pp; German.
XX
CC The present sequence codes for a Met residue followed by the 198 amino
CC acid long hMn-SOD mature polypeptide having a Lys residue at position 29.
CC The cDNA can be inserted into expression vectors containing appropriate
CC signal sequences, etc. for expression of recombinant hMn-SOD. The N-
CC terminal Met residue can be removed, e.g. by treatment with CNBr or CNCl.
CC Mature hMn-SOD is useful for treating, preventing or diagnosing
CC inflammatory, degenerative, neoplastic and rheumatic disorders; in wound
CC healing and in autoimmune diseases. (Updated on 25-MAR-2003 to correct PF
CC field.)
XX
SQ Sequence 600 BP; 173 A; 134 C; 150 G; 143 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 0.000917 Length: 600
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0
DB: 2
US-09-987-190-2 (1-30) x AAQ94271 (1-600)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSercly 20
Db 4 AAGCACTCTTGGCAGACTTGCATACGACTACGCTGCTAGAACACACATCATGCT 63
QY 21 GlnIleAsnGluIle***TyrThr 28
Db 64 CAAATCATGCATTCACACACTCT 87
RESULT 29
AAQ94272
ID AAQ94272 standard; cDNA; 600 BP.
XX
AC AAQ94272;
XX
DT 25-MAR-2003 (revised)
DT 17-MAY-1996 (first entry)
XX
DE Human manganese superoxide dismutase (Gln29) coding sequence.
XX
KM hMn-SOD; manganese; superoxide dismutase; tetramer; inflammation;
KM autoimmune disease; rheumatoid arthritis; neoplasm; emphysema;
KM osteoarthritis; wound healing; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH CDS 1..600
FT

```

FT      /*tag= a
FT      /product= "Met_hmn-SOD (Gln29)"
XX
XX      EP676472-A1.
XX
XX      11-OCT-1995.
XX
XX      10-MAR-1998; 95EP-00107460.
XX
XX      14-MAR-1987; 87DE-03708306.
XX      26-MAY-1987; 87DE-03717695.
XX      10-JUL-1987; 87DE-03722884.
XX      24-DEC-1987; 87DE-03744038.
XX
XX      (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX
XX      Heckl K, Spevak W, Ostermann E, Zoepfel A, Krystek E,
XX      Maurer-Fogy I, Wiche-Castanon M, Stratowa C, Hauptmann R;
XX      WPI; 1995-346092/45.
XX      P-PSDB; AAR75192.
XX
XX      Genes encoding recombinant human manganese superoxide dismutase - for
XX      treatment, prevention and diagnosis of inflammatory diseases.
XX
XX      Claim 8; Page 6; 54pp; German.
XX
XX      The present sequence codes for a Met residue followed by the 198 amino
XX      acid long hmn-SOD mature polypeptide having a Gln residue at position 29.
XX      The cDNA can be inserted into expression vectors containing appropriate
XX      signal sequences, etc. for expression of recombinant hmn-SOD. The N-
XX      terminal Met residue can be removed, e.g. by treatment with CNBr or CNCl.
XX      Mature hmn-SOD is useful for treating, preventing or diagnosing
XX      inflammatory, degenerative, neoplastic and rheumatic disorders; in wound
XX      healing and in autoimmune diseases. (Updated on 25-MAR-2003 to correct PF
XX      field.)
XX
XX      SQ Sequence 600 BP; 172 A; 135 C; 150 G; 143 T; 0 U; 0 Other;
XX
XX      Alignment Scores:
XX      Pred. No.: 0.000917 Length: 600
XX      Score: 74.00 Matches: 12
XX      Percent Similarity: 78.57% Conservative: 10
XX      Best Local Similarity: 42.86% Mismatches: 6
XX      Query Match: 51.03% Indels: 0
XX      Gaps: 2
XX
XX      US-09-987-190-2 (1-30) x AAQ94272 (1-600)
XX
XX      QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
XX      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX      Db 4 AAGCAGCTCTTGCCAGACTTGCCATGACGACTAGCGTGTCTAGAACGACACATCATGCT 63
XX
XX      QY 21 GlnIleAsnGluIle***TyrThr 28
XX      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX      Db 64 CAAATCATGCAATTGCACCACTCT 87
XX
XX      RESULT 30
XX      AAQ94277
XX      ID AAQ94277 standard; cDNA; 600 BP.
XX
XX      AC AAQ94277;
XX
XX      DT 25-MAR-2003 (revised)
XX      DT 23-MAY-1996 (first entry)
XX
XX      DE Human manganese superoxide dismutase (lys29) coding sequence.
XX
XX      hmn-SOD; manganese superoxide dismutase; tetramer; inflammation;
XX      autoimmune disease; superoxide dismutase; rheumatoid arthritis; neoplasia; emphysema;
XX      osteoarthritis; wound healing; ss.
XX
XX      Homo sapiens.
XX

```

```

OS      Synthetic.
XX
XX      Key
XX      CDS
XX
XX      Location/Qualifiers
XX      1..600
XX
XX      /*tag= a
XX      /product= "Met_hmn-SOD (Lys29)"
XX      /note= "the first 31 codons are provided by a synthetic
XX      linker sequence"
XX
XX      EP676472-A1.
XX
XX      11-OCT-1995.
XX
XX      10-MAR-1998; 95EP-00107460.
XX
XX      14-MAR-1987; 87DE-03708306.
XX      26-MAY-1987; 87DE-03717695.
XX      10-JUL-1987; 87DE-03722884.
XX      24-DEC-1987; 87DE-03744038.
XX
XX      (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX
XX      Heckl K, Spevak W, Ostermann E, Zoepfel A, Krystek E,
XX      Maurer-Fogy I, Wiche-Castanon M, Stratowa C, Hauptmann R;
XX      WPI; 1995-346092/45.
XX
XX      Genes encoding recombinant human manganese superoxide dismutase - for
XX      treatment, prevention and diagnosis of inflammatory diseases.
XX
XX      Claim 8; Page 17; 54pp; German.
XX
XX      The present sequence codes for a Met residue followed by the 198 amino
XX      acid long hmn-SOD mature polypeptide having a Lys residue at position 29.
XX      The cDNA can be inserted into expression vectors containing appropriate
XX      signal sequences, etc. for expression of recombinant hmn-SOD. The N-
XX      terminal Met residue can be removed, e.g. by treatment with CNBr or CNCl.
XX      Mature hmn-SOD is useful for treating, preventing or diagnosing
XX      inflammatory, degenerative, neoplastic and rheumatic disorders; in wound
XX      healing and in autoimmune diseases. (Updated on 25-MAR-2003 to correct PF
XX      field.)
XX
XX      SQ Sequence 600 BP; 173 A; 133 C; 150 G; 144 T; 0 U; 0 Other;
XX
XX      Alignment Scores:
XX      Pred. No.: 0.000917 Length: 600
XX      Score: 74.00 Matches: 12
XX      Percent Similarity: 78.57% Conservative: 10
XX      Best Local Similarity: 42.86% Mismatches: 6
XX      Query Match: 51.03% Indels: 0
XX      Gaps: 2
XX
XX      US-09-987-190-2 (1-30) x AAQ94277 (1-600)
XX
XX      QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
XX      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX      Db 4 AAGCAGCTCTTGCCAGACTTGCCATGACGACTAGCGTGTCTAGAACGACACATCATGCT 63
XX
XX      QY 21 GlnIleAsnGluIle***TyrThr 28
XX      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX      Db 64 CAAATCATGCAATTGCACCACTCT 87
XX
XX      RESULT 31
XX      AAQ20194
XX      ID AAQ20194 standard; DNA; 609 BP.
XX
XX      AC AAQ20194;
XX
XX      DT 01-APR-1992 (first entry)
XX
XX      DE Mn-SOD (Ile59Thr).
XX
XX      Manganese superoxide dismutase; vector; anti-inflammatory; ds.
XX

```

XX Homo sapiens.
OS
XX
XX EP462836-A.
XX
XX PD 27-DEC-1991.
XX
XX PF 20-JUN-1991; 91EP-00305596.
XX
XX PR 20-JUN-1990; 90JP-00159925.
XX PR 19-OCT-1990; 90JP-00279286.
XX
XX PA (MITK) MITSUI TOATSU CHEM INC.
XX
XX PI Takahashi S, Makino T, Asanagi M, Yoshino C;
XX
XX DR WPI; 1992-001187/01.
XX DR P-PSDB; AAR20015.
XX
XX PT New recombinant vector plasmid - expresses human manganese, superoxide
XX PT dismutase, used as antiinflammatory agent.
XX
XX PS Disclosure; Fig 8; 22pp; English.
XX
XX CC A vector was constructed contg. tac/P1 ligated promoter which has this
XX CC human Mn-SOD structural gene. The gene encodes modified human Mn-SOD in
XX CC which the 59th isoleucine is converted to threonine
XX
SQ Sequence 609 BP; 171 A; 148 C; 157 G; 133 T; 0 U; 0 Other;
SO
Alignment Scores:
Pred. No.: 0.000935 Length: 609
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: Gaps: 0
US-09-987-190-2 (1-30) x AAQ20194 (1-609)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 6 AAGGACAGCCTCCCTCGACTGACCTACGACTAGCGGCCCTGGAACCTCACTCAACGCG 65
QY 21 GlnIleAsnGluIle**TyrThr 28
DB 66 CAGATCATGCAGCTGCACACACG 89
RESULT 32
ABT09580
ID ABT09580 standard; DNA; 666 BP.
XX
XX AC ABT09580;
XX
XX DT 05-DEC-2002 (first entry)
XX
XX DE Phase-1 Rat CT gene SEQ ID No 668.
XX
XX KM Rat; toxicity study; rat toxic response gene; toxicological response;
XX KM drug development; phase-1 rat CT gene; ds.
XX
XX OS Rattus sp.
XX OS
XX PN WO200266682-A2.
XX PD 29-AUG-2002.
XX
XX PF 29-JAN-2002; 2002WO-US002935.
XX
XX PR 29-JAN-2001; 2001US-0264933P.
XX PR 26-JUL-2001; 2001US-0308161P.
XX
XX PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

XX
XX PI Farris G, Hicken SH, Farr SB;
XX
XX DR WPI; 2002-674961/72.
XX
XX PT Evaluating the toxicity of an agent, useful in drug development or in
XX PT determining toxicological responses to a new drug, by determining the
XX PT expression of rat toxicologically relevant genes in the test animal in
XX PT response to the test agent.
XX
XX PS Disclosure; Page 270; 388pp; English.
XX
XX CC The invention relates to a method used for evaluating the toxicity of an
XX CC agent comprising determining the expression of a rat toxic response
XX CC gene(s) in the test animal in response to the agent. The method is useful
XX CC in drug development, particularly for conducting toxicity studies and
XX CC analysis before a new drug or compound is approved for human consumption
XX CC or use. The method is also useful in determining toxicological responses
XX CC to a new drug. This polynucleotide sequence represents a phase-1 rat CT
XX CC gene of the invention
XX
SQ Sequence 666 BP; 172 A; 164 C; 182 G; 146 T; 0 U; 2 Other;
SO
Alignment Scores:
Pred. No.: 0.00105 Length: 666
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: Gaps: 0
US-09-987-190-2 (1-30) x ABT09580 (1-666)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 88 AAGGACAGCCTCCCTCGACTGACCTACGACTATGCGCGCTGGAGCGCACATTAAACGCG 147
QY 21 GlnIleAsnGluIle**TyrThr 28
DB 148 CAGATCATGCAGCTGCACACACG 171
RESULT 33
AAZ39781
ID AAZ39781 standard; DNA; 681 BP.
XX
XX AC AAZ39781;
XX
XX DT 06-MAR-2000 (first entry)
XX
XX DE Human manganese superoxide dismutase (MnSOD) mutant protein DNA.
XX
XX KM Manganese superoxide dismutase; MnSOD; ECsOD; proteoglycan; human;
XX KM endothelial; oxidative damage; pulmonary inflammatory injury; cancer;
XX KM lung disease; hypoxia; ischemia; reperfusion injury; arthritis;
XX KM hyperoxia; atherosclerosis; lupus erythematosus; hypertension;
XX KM neutrophil-mediated inflammation; mutant; ss.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX PN WO9958547-A1.
XX PD 18-NOV-1999.
XX
XX PF 06-MAY-1999; 99WO-US009921.
XX
XX PR 08-MAY-1998; 98US-00075019.
XX
XX PA (WEBB-) WEBB-MARING INST BIOMEDICAL RES.
XX
XX PI Mccord JM, Gao B, Flores SC;
XX
XX DR WPI; 2000-062283/05.

DR P-PSDB; AAY55849.
 XX Modified manganese superoxide dismutase, methods of production and
 PT antibodies.
 XX
 PS Claim 11; Page 74-75; 83pp; English.
 XX
 CC The invention provides a nucleic acid molecule encoding a genetically
 CC modified manganese superoxide dismutase (MnSOD). The nucleic acid
 CC comprises: a first nucleic acid sequence encoding an enzymatically active
 CC portion of MnSOD; and a second nucleic acid sequence encoding a peptide
 CC (ECsOD) that binds to polyanionic polysaccharides or proteoglycans on
 CC endothelial cell surfaces. The protein protects a mammal, especially
 CC humans, from oxidative damage and especially from conditions consisting
 CC of pulmonary inflammatory injury, lung disease, cancer, hypoxia, ischemia
 CC reperfusion injury, hyperoxia, atherosclerosis, arthritis, lupus
 CC erythematosis, hypertension and neutrophil-mediated inflammation. The
 CC lung disease is infant or adult respiratory distress syndrome,
 CC interstitial lung disease or asthma. The mutant MnSOD also protects
 CC organs of mammals from pre- and post-transplantation oxidative damage.
 CC MnSOD is positively charged at physiological pH and has a longer plasma
 CC half-life of about 4 hours compared to 6-15 minutes for cytosolic Cu,Zn
 CC SOD (following intravenous injection). ECsOD has a substantial advantage
 CC over both Cu,ZnSOD and MnSOD because of its ability to bind to the
 CC endothelium. ECsOD is hard to produce in mammalian cell culture systems,
 CC so a fusion of ECsOD and MnSOD therefore overcomes these problems. The
 CC present sequence represents a DNA encoding a human MnSOD mutant protein.
 CC This comprises the MnSOD sequence, and a 78 basepair ECsOD tail-encoding
 CC fragment
 XX
 SQ Sequence 681 BP; 185 A; 170 C; 189 G; 137 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 0.00108 Length: 681
 Score: 74.00 Matches: 12
 Percent Similarity: 78.57% Conservative: 10
 Best Local Similarity: 42.86% Mismatches: 6
 Query Match: 51.03% Indels: 0
 DB: Gaps: 3
 US-09-987-190-2 (1-30) x AAZ39781 (1-681)
 QY 1 LysTyrSerIeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 Db 7 AAGCAGAGCCTCCCGACGCTGCCTACGACTACGCGCGCTCGAAGCTCACATCAACGCG 66
 QY 21 GlnIleAsnGluIle***TyrThr 28
 Db 67 CAGATCATGCGAGCTGCACACGACG 90
 RESULT 34
 AAN71370
 ID AAN71370 standard; DNA; 813 BP.
 XX
 AC AAN71370;
 XX
 DT 25-MAR-2003 (revised)
 DT 10-MAR-2003 (revised)
 DT 14-MAY-1991 (first entry)
 XX
 DE Sequence encoding human manganese superoxide dismutase.
 XX
 KM Human MSOD; hydrogen peroxide; ischaemia; lesions; inflammation;
 KM free radicals; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 43..711
 FT /*tag= a
 FT mat_peptide 115..708
 FT /*tag= b
 FT /product= "mature MSOD"

XX
 PN BE905796-A.
 XX
 PD 16-MAR-1987.
 XX
 PF 20-NOV-1986; 86BE-00905796.
 XX
 PR 22-NOV-1985; 85US-00801051.
 PR 22-NOV-1985; 85US-00801090.
 PR 12-SEP-1986; 86US-00907051.
 XX
 PA (BIOT-) BIO-TECHNOL GEN.
 XX
 DR WP1: 1987-101441/15.
 DR P-PSDB; AAN71370.
 XX
 PT New DNA coding for polypeptide of human manganese superoxidisedismutase -
 PT useful e.g. for treating inflammation, and new expression vectors and
 PT transformed cells.
 XX
 PS Disclosure; Fig 1; 46pp; French.
 XX
 CC This purified cDNA encodes both prepro- and mature-manganese superoxide
 CC dismutase (MSOD). It is one strand of a double stranded molecule
 CC contained in a recombinant vehicle. The MSOD produced catalyses the
 CC reaction of hydrogen ions and the SOD radical anion to form hydrogen
 CC peroxide and water. It is useful in veterinary and pharmaceutical
 CC compns. for e.g. reducing lesions of reperfusion following ischaemia, to
 CC prolong survival time isolated organs and for treating inflammation. See
 CC also AAN71371-72. (Updated on 10-MAR-2003 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 813 BP; 218 A; 204 C; 213 G; 178 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 0.00136 Length: 813
 Score: 74.00 Matches: 12
 Percent Similarity: 78.57% Conservative: 10
 Best Local Similarity: 42.86% Mismatches: 6
 Query Match: 51.03% Indels: 0
 DB: Gaps: 1
 US-09-987-190-2 (1-30) x AAN71370 (1-813)
 QY 1 LysTyrSerIeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 Db 115 AAGCAGAGCCTCCCGACGCTGCCTACGACTACGCGCGCTCGAAGCTCACATCAACGCG 174
 QY 21 GlnIleAsnGluIle***TyrThr 28
 Db 175 CAGATCATGCGAGCTGCACACGACG 198
 RESULT 35
 AAN81158
 ID AAN81158 standard; cDNA; 813 BP.
 XX
 AC AAN81158;
 XX
 DT 22-OCT-1990 (first entry)
 XX
 DE cDNA encoding human manganese superoxide dismutase.
 XX
 KM Human manganese superoxide dismutase; ds cDNA; oxygen free radicals.
 KM
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 43..711
 FT /*tag= a
 XX
 PN EP284105-A.
 XX
 PD 28-SEP-1988.

```
XX 25-MAR-1988; 88EP-00104880.
PF 27-MAR-1987; 87US-00032734.
XX 26-FEB-1988; 88US-00161117.
PR 26-FEB-1988; 88US-00161117.
XX (BIOT-) BIO-TECHNOLOGY GEN.
PA Hartman JR, Beck Y, Nimrod A;
XX WPI: 1988-272584/39.
DR P-PSDB; AAP80551.
XX Recombinant human manganese superoxidizedismutase - used for treating e.g.
PT reperfusion injury, inflammation, arthritis, bronchial pulmonary
PT dysplasia or lung fibrosis.
XX
PS Disclosure; Page 7; 46pp; English.
XX The cDNA encodes human manganese superoxide dismutase, and is inserted
CC into a plasmid, eg pMSB-4 (ATCC 53250)
CC
XX
SQ Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00136 Length: 813
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: Gaps: 0

US-09-987-190-2 (1-30) x AAN81158 (1-813)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 115 AAGCAGACGCTCCCGACCTGCGCTACGACTACGCGCCCGGAACCTCACATCAACGCG 174
QY 21 GlnIleAsnGluIle**TyrThr 28
Db 175 CAGATCATGCACTGCACACACAGC 198

RESULT 36
AAQ53193
ID AAQ53193 standard; cDNA; 813 BP.
XX
AC AAQ53193;
XX
DT 25-MAR-2003 (revised)
DT 21-JUN-1994 (first entry)
XX
DE MSOD cDNA.
XX
KW MSOD; manganese superoxide dismutase; N-terminal; catalyst; reperfusion;
KW injury; ischaemia; superoxide; SO; molecular oxygen; anti-inflammatory;
KW ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 43..711
FT /*tag= a
FT /*product= "MSOD"
XX
XX US270195-A.
XX 14-DEC-1993.
XX 10-JUL-1992; 92US-00912213.
XX 22-NOV-1985; 85US-00801090.
XX 12-SEP-1986; 86US-00307051.
PR 29-OCT-1986; 86IE-00002851.
```

```
ER 27-MAR-1987; 87US-00032734.
PR 13-DEC-1989; 89US-00453057.
XX
XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
PA Beck Y, Hartman JR;
XX WPI: 1993-404931/50.
DR P-PSDB; AAR44801.
XX
XX Expression plasmid in Escherichia coli host system - encodes human
PT manganese superoxidizedismutase analogue, useful for e.g. treating
PT inflammation.
XX
PS Claim 1; Fig 1a-1c; 27pp; English.
XX
CC The sequence encodes a maganese superoxide dismutase which can be used to
CC catalyse the reduction of superoxide (SO) radicals to hydrogen peroxide
CC and molecular oxygen. It can be used to reduce reperfusion injury
CC following ischaemia and prolong the survival of excised organs. It can
CC also me used as a long acting anti-inflammatory drug. (Updated on 25-MAR-
CC 2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
XX
SQ Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00136 Length: 813
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: Gaps: 0

US-09-987-190-2 (1-30) x AAQ53193 (1-813)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 115 AAGCAGACGCTCCCGACCTGCGCTACGACTACGCGCCCGGAACCTCACATCAACGCG 174
QY 21 GlnIleAsnGluIle**TyrThr 28
Db 175 CAGATCATGCACTGCACACACAGC 198

RESULT 37
AAT15589
ID AAT15589 standard; cDNA; 813 BP.
XX
AC AAT15589;
XX
DT 25-MAR-2003 (revised)
DT 06-APR-1996 (first entry)
XX
DE Human manganese superoxide-dismutase cDNA.
XX
XX Human; manganese superoxide-dismutase; T-lymphocyte; probe; cDNA;
KW Escherichia coli; plasmid pMSB-4; N-terminal truncation; cloning;
KW aminopeptidase; antiinflammatory; oxygen free radical scavenger;
KW synovial inflammation; arthritis; lung fibrosis; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 43..711
FT /*tag= a
FT /*product= "Manganese superoxide-dismutase"
FT /note= "Ec-1.15.1.1"
FT sig_peptide 43..114
FT /*tag= b
FT mat_peptide 115..708
FT /*tag= c
XX
XX EP691401-A1.
```

```

PD 10-JAN-1996.
XX
XX 25-MAR-1988; 95SEP-00106995.
XX
XX 27-MAR-1987; 87US-00032734.
XX 26-FEB-1988; 88US-00161117.
XX
XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
XX
XX Hartman JR, Beck Y, Nimrod A;
XX
XX WPI; 1996-059735/07.
XX P-PSDB; AAR90713.
XX
XX New human manganese superoxide dismutase analogues - having a Lys and
XX opt. His residue absent from the N-terminus, useful for treating e.g.
XX synovial inflammation, arthritis or lung fibrosis.
XX
XX Example 1; Fig 1; 45pp; English.
XX
XX The sequence encodes a human manganese superoxide-dismutase (MnSOD), and
XX has been isolated from a human T-lymphocyte cDNA library in phage lambda-
XX gt10 in Escherichia coli, by screening with a 5'-probe (AAT15591) and a
XX 3'-probe (AAT15592). The sequence of the insert in plasmid pMS8-4
XX (obtained by subcloning in plasmid pBR322) is shown. The cDNA may be
XX expressed in e.g. E. coli for production of recombinant MnSOD. The MnSOD
XX product may be cleaved with Aeromonas proteolytica aminopeptidase to
XX produce an N-terminally truncated analogue with lysine and optionally
XX histidine residues removed. The MnSOD analogue may be used in therapy of
XX conditions associated with generation of oxygen free radicals,
XX particularly synovial inflammation, arthritis and lung fibrosis
XX (claimed). (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 0.00136 Length: 813
XX Score: 74.00 Matches: 12
XX Percent Similarity: 78.57% Conservative: 10
XX Best Local Similarity: 42.86% Mismatches: 6
XX Query Match: 51.03% Indels: 0
XX Gaps: 0
XX
XX US-09-987-190-2 (1-30) x AAT15589 (1-813)
XX
XX QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheserAlaThrGluProTyrIleSerGly 20
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX Db 115 AAGCAGAGCCTCTCCCGACCTGCTACGACTACGGCGCCCTGGAACCTCACAACGCG 174
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX QY 21 GlnIleAsnGluIle**TyrThr 28
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX Db 175 CAGATCATGCACTGCACACGACG 198
XX
XX RESULT 38
XX AAT34277
XX ID AAT34277 standard; cDNA; 813 BP.
XX
XX AC AAT34277;
XX
XX 25-MAR-2003 (revised)
XX DT 24-OCT-1996 (first entry)
XX
XX Human manganese superoxide dismutase cDNA.
XX
XX Manganese superoxide dismutase; MnSOD; reperfusion injury; ischaemia;
XX bronchial pulmonary dysplasia; inflammation; antiinflammatory; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 43..711
XX FT /*tag= a
XX sig_peptide 43..114

```

```

FT mat_peptide /*tag= b
FT 115..708
FT /*tag= c
XX
XX US5540911-A.
XX
XX 30-JUL-1996.
XX
XX 09-JAN-1995; 95US-00370461.
XX
XX 22-NOV-1985; 85US-00801090.
XX 12-SEP-1986; 86US-00907051.
XX 29-OCT-1986; 86IE-00002851.
XX 27-MAR-1987; 87US-00032734.
XX 13-DEC-1989; 89US-00453057.
XX 10-JUL-1992; 92US-00912213.
XX 14-SEP-1993; 93US-00120951.
XX
XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
XX
XX Hartman JR, Beck Y;
XX
XX WPI; 1996-361912/36.
XX P-PSDB; AAM00018.
XX
XX Use of recombinant human manganese superoxide dismutase - for treating
XX inflammation or bronchial pulmonary dysplasia, reducing reperfusion
XX injury or prolonging organ survival.
XX
XX Claim 1; Fig 1A-1C; 27pp; English.
XX
XX A cDNA clone (AAT34277) codes for human manganese superoxide dismutase
XX (MnSOD) (AAM00018), an enzyme that catalyses the reduction of superoxide
XX radicals to H2O2 and O2. It was isolated from a human T-cell library
XX cloned into vector gt10 using probes (see also AAT34283-84) based on
XX portions of mature MnSOD. The MnSOD gene was also identified (see also
XX AAT34278-82). The cDNA can be used for the prodn. of recombinant MnSOD
XX using e.g. Escherichia coli cells as hosts. The MnSOD is useful for
XX reducing reperfusion injury, treating inflammation or bronchial pulmonary
XX dysplasia and for prolonging survival of excised organs. (Updated on 25-
XX MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR
XX field.)
XX
XX Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 0.00136 Length: 813
XX Score: 74.00 Matches: 12
XX Percent Similarity: 78.57% Conservative: 10
XX Best Local Similarity: 42.86% Mismatches: 6
XX Query Match: 51.03% Indels: 0
XX DB: 2 Gaps: 0
XX
XX US-09-987-190-2 (1-30) x AAT34277 (1-813)
XX
XX QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheserAlaThrGluProTyrIleSerGly 20
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX Db 115 AAGCAGAGCCTCTCCCGACCTGCTACGACTACGGCGCCCTGGAACCTCACAACGCG 174
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX QY 21 GlnIleAsnGluIle**TyrThr 28
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX Db 175 CAGATCATGCACTGCACACGACG 198
XX
XX RESULT 39
XX AAX24998
XX ID AAX24998 standard; cDNA; 813 BP.
XX
XX AC AAX24998;
XX
XX 05-JUL-1999 (first entry)
XX
XX Human native manganese superoxide dismutase cDNA.
XX

```

KM	Superoxide dismutase; MnSOD; SOD; human; protein engineering;
KW	enzyme engineering; antioxidant; antiinflammation; cytotoxicity;
KX	inflammation; reperfusion injury; therapy; ss.
XX	Homo sapiens.
OS	
XX	
FH	Key Location/Qualifiers
FT	CDS
FT	/tag= a
FT	sig_peptide
FT	mat_peptide
FT	/tag= b
FT	/tag= c
XX	
EN	M09913088-A1.
PD	18-MAR-1999.
XX	
PF	10-SEP-1998; 98WO-US018842.
PR	10-SEP-1997; 9TUS-00927230.
XX	(UYFL) UNITV FLORIDA.
PA	Nick HS, Silverman DN;
PI	MDI; 1999-229242/19.
DR	P-PsDB; AAW98169.
XX	
PT	New recombinant human manganese superoxide dismutase proteins.
PS	Disclosure; Page 52-53; 61pp; English.
XX	
CC	This cDNA sequence codes for human manganese superoxide dismutase
CC	(hmnsod, see AAW98169). Novel hmnsod proteins having catalytic activity
CC	which differs from this natural hmnsod are claimed. The modified proteins
CC	exhibit reduced or no product inhibition, or have greater activity, or
CC	both, compared to natural hmnsod. The modifications involve one or amino
CC	acid substitutions within the active site of the enzyme, especially at
CC	His-163 (see also AAW98171-77). Nucleic acids encoding the modified
CC	hmnsod proteins are also claimed. The modified hmnsod proteins, or
CC	expression vectors in which modified hmnsod nucleic acid is linked to a
CC	promoter (preferably mammalian), can be used to protect a cell line from
CC	damage caused by superoxide radicals (claimed). They can also be used to
CC	treat subjects suffering from, or at risk of, cytotoxicity caused by
CC	superoxide radicals (claimed). As such, they can be used as antioxidants
CC	in the treatment of a variety of disorders, including inflammation
CC	(claimed), reperfusion injury following ischemia (claimed), and cellular
CC	damage caused by chemotherapeutic agents
XX	
SQ	Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;
XX	
Alignment Scores:	
Pred. No.:	Score: 0.00136 Length: 813
Percent Similarity:	74.00 Matches: 12
Best Local Similarity:	78.57% Conservative: 10
Query Match:	42.86% Mismatches: 6
DB:	51.03% Indels: 0
	Gaps: 0
US-09-987-190-2 (1-30) x AAX24998 (1-813)	
QY	1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSecrly 20
Db	115 AAGCAGACGGCTCCCCCACTGCCCGCCTTCAGACTACGGCGCCCTGGAACCTCACATCAAGCG 174
QY	21 GluIleasnGluIle**TyrThr 28
Db	175 CAGATCATGCAGCTGCACCAACAGC 198
RESULT: 40	
AAG3891	

ID	AA63891 standard; cDNA: 813 BP.
AC	AAA63891;
XX	
XX	04-DEC-2000 (first entry)
DT	
XX	cDNA encoding a human manganese superoxide dismutase.
DE	
XX	Human; manganese superoxide dismutase; hmn SOD; superoxide radical;
KW	superoxide radical damage; cytotoxicity; inflammation; ischemia;
KW	reperfusion injury; ss.
XX	
OS	Homo sapiens.
FT	
FT	Key
FT	CDS
FT	location/Qualifiers
FT	43..711
FT	/tag= a
FT	/transl_except= (pos: 505..507, aa: Xaa)
FT	/transl_except= (pos: 511..513, aa: Ala)
FT	/product= "manganese superoxide dismutase"
FT	/note= "Xaa is Gln or Glu"
FT	sig_peptide
FT	43..114
FT	/tag= b
FT	115..708
FT	mat_peptide
FT	/tag= c
XX	
PN	US6107070-A.
PD	
PD	22-AUG-2000.
XX	
PF	10-SEP-1998; 98US-00151052.
XX	
PR	10-SEP-1997; 97US-00927230.
XX	
PA	(UYFL) UNIV FLORIDA.
PI	Silverman DN, Nick HS;
DR	WPI; 2000-578537/54.
DR	P-PsDB; AAB08204.
XX	
PT	Novel human manganese superoxide dismutase protein useful as antioxidant
PT	for treating cytotoxicity caused by superoxide radicals, inflammation and
PT	reperfusion injury following ischemia.
PS	Disclosure: Col 25-26; 27pp; English.
XX	
CC	The present sequence encodes a human manganese superoxide dismutase
CC	protein (hmn SOD). The specification describes a modified hmn SOD which
CC	has a catalytic activity which differs from natural hmn SOD in that it
CC	exhibits reduced or no product inhibition compared to natural hmn SOD.
CC	The natural hmn SOD is especially modified with one or more substitutions
CC	in amino acids 26, 30, 34, 74, 143, 159, 161 and 163. The modified hmn
CC	SOD is useful for protecting a cell from damage caused by superoxide
CC	radicals and for treating a subject suffering from cytotoxicity caused by
CC	superoxide radicals. The protein is useful for treating inflammation and
CC	reperfusion injury following ischemia
XX	
SQ	Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;
Alignment Scores:	
Pred. No.:	0.00136 Length: 813
Score:	74.00 Matches: 12
Percent Similarity:	78.57% Conservative: 10
Best Local Similarity:	42.86% Mismatches: 6
Query Match:	51.03% Indels: 0
DB:	Gaps: 0
US-09-987-190-2 (1-30) x AAA63891 (1-813)	
OY	1 LysTyrSerLeuProGluIleuAspTryrGluPheSerAlaThrGluProTyrlleSergly 20
Db	::: ::: ::: ::: ::: ::: ::: ::: 115 AAGCAcAGGCTCCCGAcCTGCCTCAGCATAGGGCGCCCTGGAACTCAGATCAAGCGC 174

Qy 21 Glnleangluile**TyrThr 28
|||
Db 175 CAGATCATGTCAGCTGCACACAGC 198
::: :::

Search completed: August 31, 2004, 18:17:57
Job time : 440 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 31, 2004, 20:09:53 ; Search time 408 Seconds

(without alignments)
361.870 Million cell updates/sec

Title: US-09-987-190-2
Perfect score: 145
Sequence: 1 KXSLPELDHFFSATEPEYSGQINEIXYTX 30

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Delop 6.0 , Delext 7.0

Searched: 3237270 seqs, 2460713050 residues

Total number of hits satisfying chosen parameters: 6474540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO.spool/US09987190.rnat 24082004.161332.24850/app.query.fasta_1.199
-DB=Published Applications NA -QFMT=fastcap -SUPPLX=trpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cgi -LIST=45 -DOCALLIGN=200 -THR SCORE=ext -HEAPSIZE=500 -MINLEN=0
-THR_MIN=0 -ALIGN=40 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09987190 @CGN 1.1 520 @rnat 24082004.161332.24850
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOC=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
Published Applications NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	79	54.5	812	15	US-10-109-670-4	Sequence 4, Appl
2	79	54.5	2217	13	US-10-424-599-90403	Sequence 90403, A
3	77	53.1	600	9	US-09-738-626-3227	Sequence 3227, Ap
4	77	53.1	987	13	US-10-424-599-90405	Sequence 90405, A
5	77	53.1	1143	9	US-09-818-564-1	Sequence 1, Appl
6	77	53.1	3309400	9	US-09-738-626-1	Sequence 1, Appl
7	74	51.0	224	9	US-09-960-352-5895	Sequence 5895, Ap
8	74	51.0	325	9	US-09-960-352-5895	Sequence 3021, Ap
9	74	51.0	325	9	US-09-960-352-5895	Sequence 11, Appl
10	74	51.0	424	9	US-09-960-352-5895	Sequence 14744, A
11	74	51.0	552	17	US-10-752-791-1	Sequence 1, Appl
12	74	51.0	666	17	US-10-404-460-256	Sequence 256, Ap
13	74	51.0	829	17	US-10-641-643-1348	Sequence 1348, Ap
14	74	51.0	972	14	US-10-044-090-835	Sequence 836, Ap
15	74	51.0	996	15	US-10-398-846-13503	Sequence 13503, A
16	74	51.0	1026	9	US-09-954-456-1822	Sequence 1822, Ap
17	74	51.0	1026	13	US-10-342-887-509	Sequence 509, Ap
18	74	51.0	1026	13	US-10-342-887-509	Sequence 1905, Ap
19	74	51.0	1026	13	US-10-172-118-509	Sequence 509, Ap
20	74	51.0	1026	13	US-10-172-118-509	Sequence 1905, Ap
21	74	51.0	1026	17	US-10-717-597-53	Sequence 53, Appl
22	74	51.0	1067	10	US-09-971-4298-22	Sequence 22, Appl
23	74	51.0	1452	9	US-09-917-800A-1627	Sequence 1627, Ap
24	74	51.0	1984	13	US-10-342-887-267	Sequence 267, Ap
25	74	51.0	1984	13	US-10-172-118-267	Sequence 13787, A
26	74	51.0	2825	15	US-10-198-846-13787	Sequence 42032, A
27	72	49.7	303	13	US-10-424-599-42032	Sequence 699, Ap
28	71	49.0	254	12	US-09-732-627A-699	Sequence 6936, Ap
29	71	49.0	635	17	US-10-021-323-6936	Sequence 8, Appl
30	71	49.0	721	9	US-09-987-190-8	Sequence 745, Ap
31	70	48.3	817	9	US-09-770-445-745	Sequence 1, Appl
32	70	48.3	1230025	16	US-10-289-762-1	Sequence 5397, Ap
33	68	46.9	6339	15	US-10-156-761-5397	Sequence 1, Appl
34	68	46.9	2731748	17	US-10-297-455A-1	Sequence 1, Appl
35	68	46.9	9025608	15	US-10-156-761-1	Sequence 6, Appl
36	67	46.2	597	9	US-09-727-8558-6	Sequence 294, Ap
37	67	46.2	1295	16	US-10-310-154-294	Sequence 1, Appl
38	67	46.2	1830121	15	US-10-329-960-1	Sequence 1, Appl
39	67	46.2	1830121	16	US-10-329-960-1	Sequence 4, Appl
40	66	45.5	669	9	US-09-727-8558-4	Sequence 2052, Ap
41	66	45.5	838	9	US-09-974-300-2052	Sequence 3, Appl
42	62	42.8	728	15	US-10-109-670-3	Sequence 425, Ap
43	62	42.8	767	9	US-09-070-927A-425	Sequence 122, Ap
44	61	42.1	894	15	US-10-247-671-122	Sequence 1367, Ap
45	61	42.1	1235	16	US-10-398-221-1367	

ALIGNMENTS

RESULT 1
US-10-109-670-4
; Sequence 4, Application US/10109670
; Publication No. US20030105283A1
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUO et al.
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA
; FILE REFERENCE: 1422-0523P
; CURRENT APPLICATION NUMBER: US/10/109,670
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 4
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Malassezia furfur
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(812)
; OTHER INFORMATION: Strandedness:double-Topology:linear-Molecule Type:cDNA to mRNA
US-10-109-670-4

Alignment Scores: 9.82e-05 Length: 812
Pred. No.: 9.82e-05

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Score: 79.00 Matches: 15
Percent Similarity: 70.37% Conservative: 4
Best Local Similarity: 55.56% Mismatches: 8
Query Match: 54.48% Indels: 0
DB: 15 Gaps: 0
US-09-987-190-2 (1-30) x US-10-109-670-4 (1-812)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
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QY 21 GluIleAsnGluIle**Tyr 27
DB 134 GAGATCATGGAGACGACACTAC 154

RESULT 2
US-10-424-599-90403
; Sequence 90403, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 90403
; LENGTH: 2217
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_52646C.1
US-10-424-599-90403

Alignment Scores:
Pred. No.: 0.000362 Length: 2217
Score: 79.00 Matches: 13
Percent Similarity: 80.77% Conservative: 8
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 54.48% Indels: 0
DB: 13 Gaps: 0
US-09-987-190-2 (1-30) x US-10-424-599-90403 (1-2217)

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DB 1142 TACAGCGCTCCCGATCTGGATTCGACTATGCGCTCTCGAGCCAGCCATCAGCGCGGAA 1201
QY 22 IleAsnGluIle**Tyr 27
DB 1202 ATCATGACGCTGCACAC 1219

RESULT 3
US-09-738-626-3227
; Sequence 3227, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAMA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
```

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; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3227
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3227

Alignment Scores:
Pred. No.: 0.000156 Length: 600
Score: 77.00 Matches: 13
Percent Similarity: 74.07% Conservative: 7
Best Local Similarity: 48.15% Mismatches: 7
Query Match: 53.10% Indels: 0
DB: 9 Gaps: 0
US-09-987-190-2 (1-30) x US-09-738-626-3227 (1-600)

QY 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 21
DB 10 TACGAACCTCCCAAGACTCGATCGCATACGACGCTCTCGAGCCACACATCGCCGCTGAA 69
QY 22 IleAsnGluIle**TyrThr 28
DB 70 ATCATGACGCTTCACCACTCC 90

RESULT 4
US-10-424-599-90405/C
; Sequence 90405, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 90405
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_52648C.1
US-10-424-599-90405

Alignment Scores:
Pred. No.: 0.000298 Length: 987
Score: 77.00 Matches: 13
Percent Similarity: 76.92% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 6
Query Match: 53.10% Indels: 0
DB: 13 Gaps: 0
US-09-987-190-2 (1-30) x US-10-424-599-90405 (1-987)

QY 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 21
DB 805 TACAGCGCTCCCGATCTGGATTCGACTATGCGCACTCGAGCCAGCCATCAGCGCGGAC 746
QY 22 IleAsnGluIle**Tyr 27
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Db          745 ATCATGCGACTTCACCACTCC 728
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          :||          :||
RESULT 5
US-09-818-564-1
; Sequence 1, Application US/09818564
; Patent No. US20020137151A1
; GENERAL INFORMATION:
; APPLICANT: MERRIAM, MORIEL
; APPLICANT: GUYONVARCH, ARNEL
; APPLICANT: MAXX, ACHIT
; TITLE OF INVENTION: A PROCESS FOR THE FERMENTATIVE PREPARATION OF METABOLIC
; TITLE OF INVENTION: PRODUCTS AND FOR THE NUCLEOTIDE SEQUENCES ENCODING FOR
; FILE REFERENCE: 21123/27841/MAS
; CURRENT APPLICATION NUMBER: US/09/818,564
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 09/373,731
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Corynebacterium melassecola
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (338)..(937)
; OTHER INFORMATION: ATCC 17965
US-09-818-564-1

Alignment Scores:
Pred. No.: 0.000361      Length: 1143
Score: 77.00             Matches: 13
Percent Similarity: 74.07% Conservative: 7
Best Local Similarity: 48.15% Mismatches: 7
Query Match: 53.10%      Indels: 0
                        Gaps: 0
                        DB:

US-09-987-190-2 (1-30) x US-09-818-564-1 (1-1143)

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          |||          :||
          :||          :||
Db          347 TACGAACCTCCAGAACCTTCGACTACGACGCTTCGAGCCACATCGCGCTGAA 406
          |||          :||
          :||          :||
Cy          22 lleaengIuile***TyTThr 28
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          :||          :||
Db          407 ATCATGAGCTTCACCACTCC 427
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          :||          :||

RESULT 6
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: IATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/37484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
```

```
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Alignment Scores:
Pred. No.: 11.3          Length: 3309400
Score: 77.00             Matches: 13
Percent Similarity: 74.07% Conservative: 7
Best Local Similarity: 48.15% Mismatches: 7
Query Match: 53.10%      Indels: 0
                        Gaps: 0
                        DB:

US-09-987-190-2 (1-30) x US-09-738-626-1 (1-3309400)

Cy          2 TyTserleupProgluleuAspTyTgIupheserAlaThrGluProTyTIlleSergIyGln 21
          |||          :||
          :||          :||
Db          3126401 TACGAACCTCCAGAACCTTCGACTACGACGCTTCGAGCCACATCGCGCTGAA 3126460
          |||          :||
          :||          :||
Cy          22 lleaengIuile***TyTThr 28
          |||          :||
          :||          :||
Db          3126461 ATCATGAGCTTCACCACTCC 3126481
          |||          :||
          :||          :||

RESULT 7
US-09-960-352-5895
; Sequence 5895, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Byatt, John C.
; APPLICANT: Machialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 5895
; LENGTH: 224
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 25-LIB34-057-Q1-E1-G1
US-09-960-352-5895

Alignment Scores:
Pred. No.: 0.000157      Length: 224
Score: 74.00             Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03%      Indels: 0
                        Gaps: 0
                        DB:

US-09-987-190-2 (1-30) x US-09-960-352-5895 (1-224)

Cy          1 LysTyTserleupProgluleuAspTyTgIupheserAlaThrGluProTyTIlleSergIy 20
          |||          :||
          :||          :||
Db          140 AAGCACAGCCTCCCGGACCTCCGCTACGACTACGCGGCGCTGAGCGGACATCAACGCG 199
          |||          :||
          :||          :||
Cy          21 GlnlleaengIuile***TyTThr 28
          |||          :||
          :||          :||
Db          200 CAGATCATGCGCTTCACCACTCC 223
          |||          :||
          :||          :||

RESULT 8
US-09-960-352-3021
; Sequence 3021, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
```

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; APPLICANT: Tao, Nengping
; APPLICANT: Byatt, John C.
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 3021
; LENGTH: 259
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 13-LIB34-076-Q1-E1-D1
US-09-960-352-3021

Alignment Scores:
Pred. No.: 0.00019 Length: 259
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: Gaps: 0

US-09-987-190-2 (1-30) x US-09-960-352-3021 (1-259)

QY 1 LysTySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 142 AAGCAGACGCTCCCGACCTGCGCTACGACTACGCGCCCTGGAGCCGCACTCAACCG 201
21 GlnIleAsnGluile**TyrThr 28
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 202 CAGATCATGCACTGCACACACAGC 225

RESULT 9
US-09-993-333-11
; Sequence 11, Application US/09993333
; Patent No. US20020156040A1
; GENERAL INFORMATION:
; APPLICANT: Oberley, Larry Wayne
; APPLICANT: Weydert, Christine J.
; APPLICANT: Smith, Benjamin Barnes
; TITLE OF INVENTION: Reduction of antioxidant enzyme levels in tumor cells using antis
; FILE REFERENCE: 875.042US1
; CURRENT FILING DATE: 2001-11-14
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/248,328
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-993-333-11

Alignment Scores:
Pred. No.: 0.000255 Length: 325
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: Gaps: 0

US-09-987-190-2 (1-30) x US-09-993-333-11 (1-325)

QY 1 LysTySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 113 AAGCAGACGCTCCCGACCTGCGCTACGACTACGCGCCCTGGAGCCGCACTCAACCG 172
21 GlnIleAsnGluile**TyrThr 28
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 21 GlnIleAsnGluile**TyrThr 28
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB: Gaps: 0
```

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Db 173 CAGATCATGCACTGCACACACAGC 196

RESULT 10
US-09-960-352-14744
; Sequence 14744, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengping
; APPLICANT: Byatt, John C.
; APPLICANT: Machialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 14744
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 63-LIB3057-022-Q1-K1-H4
US-09-960-352-14744

Alignment Scores:
Pred. No.: 0.00036 Length: 424
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: Gaps: 0

US-09-987-190-2 (1-30) x US-09-960-352-14744 (1-424)

QY 1 LysTySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 AAGCAGACGCTCCCGACCTGCGCTACGACTACGCGCCCTGGAGCCGCACTCAACCG 180
21 GlnIleAsnGluile**TyrThr 28
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 CAGATCATGCACTGCACACACAGC 204

RESULT 11
US-10-752-791-1
; Sequence 1, Application US/10752791
; Publication No. US20040152115A1
; GENERAL INFORMATION:
; APPLICANT: Anziano, Paul Q.
; TITLE OF INVENTION: Manganese Superoxide Dismutase Exon 3-Deleted Isoforms
; FILE REFERENCE: 53073-0001-US
; CURRENT FILING DATE: 2004-01-07
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US/09/623,025C
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: PCT/US99/04129
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(552)
; OTHER INFORMATION: Isoform of MnSOD E3(-)
US-10-752-791-1

Alignment Scores:
Pred. No.: 0.000508 Length: 552
```

Score:	74.00	Matches:	12
Percent Similarity:	78.57%	Conservative:	10
Best Local Similarity:	42.86%	Mismatches:	6
Query Match:	51.03%	Indels:	0
DB:	17	Gaps:	0

```

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020137051A1 010001CB1
US-10-044-090-836

Alignment Scores:
Pred. No.: 0.00106 Length: 972
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 14 Gaps: 0

US-09-987-190-2 (1-30) x US-10-044-090-836 (1-972)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 20
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 166 AAGCAGACGCTCCCGACCTGCGCTACGACTACGGCGCCCTGGAACTCAGATCAACGCG 225
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

QY 21 GlnIleAsnGluIle***TyrThr 28
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 226 CAGATCATGCAGCTGCACCAACGACG 249
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

RESULT 15
US-10-198-846-13503
; Sequence 13503, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13503
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-13503

Alignment Scores:
Pred. No.: 0.00109 Length: 996
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 15 Gaps: 0

US-09-987-190-2 (1-30) x US-10-198-846-13503 (1-996)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 20
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 163 AAGCAGACGCTCCCGACCTGCGCTACGACTACGGCGCCCTGGAACTCAGATCAACGCG 225
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

QY 21 GlnIleAsnGluIle***TyrThr 28
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 223 CAGATCATGCAGCTGCACCAACGACG 246
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

RESULT 16
US-09-954-456-1822
; Sequence 1822, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul

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TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer
FILE OF INVENTION: Sets
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIORITY APPLICATION NUMBER: US/60/233,617
PRIORITY FILING DATE: 2000-09-18
PRIORITY APPLICATION NUMBER: US/60/234,052
PRIORITY FILING DATE: 2000-09-20
PRIORITY APPLICATION NUMBER: US/60/234,923
PRIORITY FILING DATE: 2000-09-25
PRIORITY APPLICATION NUMBER: US/60/235,134
PRIORITY FILING DATE: 2000-09-25
PRIORITY APPLICATION NUMBER: US/60/235,637
PRIORITY FILING DATE: 2000-09-26
PRIORITY APPLICATION NUMBER: US/60/235,638
PRIORITY FILING DATE: 2000-09-26
PRIORITY APPLICATION NUMBER: US/60/235,711
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: US/60/235,720
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: US/60/235,840
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: US/60/235,863
PRIORITY FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1822
LENGTH: 1026
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-1822

Alignment Scores:
Pred. No.: 0.00114 Length: 1026
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 9 Gaps: 0
US-09-987-190-2 (1-30) x US-09-954-456-1822 (1-1026)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerLanThrGluProTyrIleSerGly 20
|||||
Db 77 AAGCAGAGCGCTCCGCCGACCTGCGACTACGCGCGCCCTGGAACCTGACATCAACGCG 136
QY 21 GlnIleAsnGluIle**TyrThr 28
|||||
Db 137 CAGATCATGCACTGCACCAACAGC 160

RESULT 17
US-10-342-887-509
; Sequence 509, Application US/10/342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/360,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118

```

```
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 509
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-509

Alignment Scores:
Pred. No.: 0.00114 Length: 1026
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 13 Gaps: 0

US-09-987-190-2 (1-30) x US-10-342-887-509 (1-1026)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPhseSerAlaThrGluProTyrIleSerGly 20
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 77 AAGCAGACGCTCCCGACCTGCTACGACTACGCGCCCTGGAACTCAGATCAACGCG 136
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 21 GlnIleAsnGluIle**TyrThr 28
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 137 CAGATCATGCGAGCTGCACCAACGAC 160
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 18
US-10-342-887-1905
; Sequence 1905, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1905
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1905

Alignment Scores:
Pred. No.: 0.00114 Length: 1026
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 13 Gaps: 0

US-09-987-190-2 (1-30) x US-10-342-887-1905 (1-1026)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPhseSerAlaThrGluProTyrIleSerGly 20
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 77 AAGCAGACGCTCCCGACCTGCTACGACTACGCGCCCTGGAACTCAGATCAACGCG 136
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 21 GlnIleAsnGluIle**TyrThr 28
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 137 CAGATCATGCGAGCTGCACCAACGAC 160
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
RESULT 19
US-10-172-118-509
; Sequence 509, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 509
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-172-118-509

Alignment Scores:
Pred. No.: 0.00114 Length: 1026
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 13 Gaps: 0

US-09-987-190-2 (1-30) x US-10-172-118-509 (1-1026)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPhseSerAlaThrGluProTyrIleSerGly 20
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 77 AAGCAGACGCTCCCGACCTGCTACGACTACGCGCCCTGGAACTCAGATCAACGCG 136
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 21 GlnIleAsnGluIle**TyrThr 28
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 137 CAGATCATGCGAGCTGCACCAACGAC 160
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 20
US-10-172-118-1905
; Sequence 1905, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1905
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-172-118-1905
```



```
/ SEQ ID NO 1627
/ LENGTH: 1492
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
/ FEATURE:
/ OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_017051
US-09-917-800A-1627

Alignment Scores:
Pred. No.: 0.00185 Length: 1492
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x US-09-917-800A-1627 (1-1492)

QY 1 LysTySerLeuProGluIleuAspTyrgluPheserAlathrgluProTyrlleserGly 20
Db 141 AAGCAGAGCTCTCCCTGACCTGCTTACGACTATGCGCGCTGAGCGCACATTAACGCG 200
QY 21 GlnIleAsnGluIle**TyThr 28
Db 201 CAGATCATGCAGCTGCACCCACG 224

RESULT 24
US-10-342-887-267
/ Sequence 267, Application US/10342887
/ Publication No. US20040058340A1
/ GENERAL INFORMATION:
/ APPLICANT: Dai, Hongyue
/ APPLICANT: Linsley, Peter S.
/ APPLICANT: Mao, Mao
/ APPLICANT: Roberts, Christopher J.
/ APPLICANT: Van 't Veer, Laura Johanna
/ APPLICANT: Van de Vijver, Marc J.
/ APPLICANT: Bernards, Rene
/ TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
/ FILE REFERENCE: 9301-188-999
/ CURRENT APPLICATION NUMBER: US/10/342,887
/ CURRENT FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: 60/298,918
/ PRIOR FILING DATE: 2001-06-18
/ PRIOR APPLICATION NUMBER: 60/380,710
/ PRIOR FILING DATE: 2002-05-14
/ PRIOR APPLICATION NUMBER: 10/172,118
/ PRIOR FILING DATE: 2002-06-14
/ NUMBER OF SEQ ID NOS: 2699
/ SEQ ID NO 267
/ LENGTH: 1984
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-342-887-267

Alignment Scores:
Pred. No.: 0.00267 Length: 1984
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 13 Gaps: 0

US-09-987-190-2 (1-30) x US-10-342-887-267 (1-1984)

QY 1 LysTySerLeuProGluIleuAspTyrgluPheserAlathrgluProTyrlleserGly 20
Db 150 AAGCAGAGCTCTCCCTGACCTGCTTACGACTATGCGCGCTGAGCGCACATTAACGCG 209
QY 21 GlnIleAsnGluIle**TyThr 28
Db 210 CAGATCATGCAGCTGCACCCACG 233
```

```
RESULT 25
US-10-172-118-267
/ Sequence 267, Application US/10172118
/ Publication No. US20030224374A1
/ GENERAL INFORMATION:
/ APPLICANT: Dai, Hongyue
/ APPLICANT: Linsley, Peter
/ APPLICANT: Mao, Mao
/ APPLICANT: Roberts, Chris
/ APPLICANT: Van 't Veer, Laura
/ APPLICANT: Van de Vijver, Marc
/ APPLICANT: Bernards, Rene
/ TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
/ FILE REFERENCE: 9301-175-999
/ CURRENT APPLICATION NUMBER: US/10/172,118
/ CURRENT FILING DATE: 2002-06-14
/ PRIOR APPLICATION NUMBER: 60/380,770
/ PRIOR FILING DATE: 2002-05-14
/ NUMBER OF SEQ ID NOS: 2699
/ SEQ ID NO 267
/ LENGTH: 1984
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ PUBLICATION INFORMATION:
/ DATABASE ACCESSION NUMBER: AL050388
/ DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-267

Alignment Scores:
Pred. No.: 0.00267 Length: 1984
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 13 Gaps: 0

US-09-987-190-2 (1-30) x US-10-172-118-267 (1-1984)

QY 1 LysTySerLeuProGluIleuAspTyrgluPheserAlathrgluProTyrlleserGly 20
Db 150 AAGCAGAGCTCTCCCTGACCTGCTTACGACTATGCGCGCTGAGCGCACATTAACGCG 209
QY 21 GlnIleAsnGluIle**TyThr 28
Db 210 CAGATCATGCAGCTGCACCCACG 233

RESULT 26
US-10-198-846-13787
/ Sequence 13787, Application US/10198846
/ Publication No. US2003009974A1
/ GENERAL INFORMATION:
/ APPLICANT: Lillie, James
/ APPLICANT: Xu, Yongyao
/ APPLICANT: Wang, Youzhen
/ APPLICANT: Steinmann, Kathleen
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
/ TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
/ FILE REFERENCE: MRI-049
/ CURRENT APPLICATION NUMBER: US/10/198,846
/ CURRENT FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/306,220
/ PRIOR FILING DATE: 2001-07-18
/ NUMBER OF SEQ ID NOS: 14084
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13787
/ LENGTH: 2825
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-198-846-13787
```

Db 245 ATCATGCACTCCATCAC 262

```
RESULT 30
US-09-987-190-8
; Sequence 8, Application US/09987190
; Patent No. US20020058293A1
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, Kazutosh
; APPLICANT: MIZUTANI, Shigetoshi
; APPLICANT: ENDO, Masahiro
; APPLICANT: KATO, Ikumoshin
; TITLE OF INVENTION: FUNGAL ANTIGENS AND PROCESS FOR PRODUCING THE SAME
; FILE REFERENCE: 1422-0502P
; CURRENT APPLICATION NUMBER: US/09/987,190
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/262,856
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 721
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-987-190-8

Alignment Scores:
Pred. No.: 0.0026 Length: 721
Score: 71.00 Matches: 13
Percent Similarity: 93.75% Conservative: 2
Best Local Similarity: 81.25% Mismatches: 1
Query Match: 48.97% Indels: 0
Gaps: 0

US-09-987-190-2 (1-30) x US-09-987-190-8 (1-721)

QY 13 AlaThrluProTyrIleSerGlyGlnIleasnGluIle***TyrThr 28
Db 1 GCCACTGACCGTATCATCAGGACGACAAATGACGAATTCATCTACCT 48

RESULT 31
US-09-770-445-745
; Sequence 745, Application US/09770445
; Patent No. US20020023281A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Mathew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Moesener, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maya
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2023US (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 745
; LENGTH: 817
```

```
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-445-745

Alignment Scores:
Pred. No.: 0.00469 Length: 817
Score: 70.00 Matches: 12
Percent Similarity: 76.92% Conservative: 8
Best Local Similarity: 46.15% Mismatches: 6
Query Match: 48.28% Indels: 0
Gaps: 0

US-09-987-190-2 (1-30) x US-09-770-445-745 (1-817)

QY 2 TyrSerIeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 48 TTACGCTTCCTGATCTTCCTTACGATTAATGCGCATTTGAAACGGCCATTAGTGAGAG 107

QY 22 IleasnGluIle***Tyr 27
Db 108 ATCATGCAATTCATCAC 125

RESULT 32
US-10-289-762-1
; Sequence 1, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(15000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15001)..(30000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (30001)..(45000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (45001)..(60000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (60001)..(75000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (75001)..(90000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (90001)..(105000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (105001)..(120000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
```

LOCATION: (120001)..(135000)	OTHER INFORMATION: n=a or c or g or t
FEATURE:	
NAME/KEY: misc feature	LOCATION: (405001)..(420000)
OTHER INFORMATION: n=a or c or g or t	
FEATURE:	
NAME/KEY: misc feature	LOCATION: (420001)..(435000)
OTHER INFORMATION: n=a or c or g or t	
FEATURE:	
NAME/KEY: misc feature	LOCATION: (435001)..(450000)
OTHER INFORMATION: n=a or c or g or t	
FEATURE:	
NAME/KEY: misc feature	LOCATION: (450001)..(465000)
OTHER INFORMATION: n=a or c or g or t	
FEATURE:	
NAME/KEY: misc feature	LOCATION: (465001)..(480000)
OTHER INFORMATION: n=a or c or g or t	
FEATURE:	
NAME/KEY: misc feature	LOCATION: (480001)..(495000)
OTHER INFORMATION: n=a or c or g or t	
FEATURE:	
NAME/KEY: misc feature	LOCATION: (495001)..(510000)
OTHER INFORMATION: n=a or c or g or t	
FEATURE:	
NAME/KEY: misc feature	LOCATION: (510001)..(525000)
OTHER INFORMATION: n=a or c or g or t	
FEATURE:	
NAME/KEY: misc feature	LOCATION: (525001)..(540000)
OTHER INFORMATION: n=a or c or g or t	
FEATURE:	
NAME/KEY: misc feature	LOCATION: (540001)..(555000)
OTHER INFORMATION: n=a or c or g or t	
FEATURE:	
NAME/KEY: misc feature	LOCATION: (555001)..(570000)
OTHER INFORMATION: n=a or c or g or t	
FEATURE:	
NAME/KEY: misc feature	LOCATION: (570001)..(585000)
OTHER INFORMATION: n=a or c or g or t	
FEATURE:	
NAME/KEY: misc feature	LOCATION: (585001)..(600000)
OTHER INFORMATION: n=a or c or g or t	
FEATURE:	
NAME/KEY: misc feature	LOCATION: (600001)..(615000)
OTHER INFORMATION: n=a or c or g or t	
FEATURE:	
NAME/KEY: misc feature	LOCATION: (615001)..(630000)
OTHER INFORMATION: n=a or c or g or t	
FEATURE:	
NAME/KEY: misc feature	LOCATION: (630001)..(645000)
OTHER INFORMATION: n=a or c or g or t	
FEATURE:	
NAME/KEY: misc feature	LOCATION: (645001)..(660000)
OTHER INFORMATION: n=a or c or g or t	
FEATURE:	
NAME/KEY: misc feature	LOCATION: (660001)..(675000)
OTHER INFORMATION: n=a or c or g or t	

```

; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (675001)..(690000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:

Alignment Scores:
Pred. No.: 62.9 Length: 1230025
Score: 70.00 Matches: 13
Percent Similarity: 76.19% Conservative: 3
Best Local Similarity: 61.90% Mismatches: 5
Query Match: 48.28% Indels: 0
DB: 16 Gaps: 0

US-09-987-190-2 (1-30) x US-10-289-762-1 (1-1230025)

QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlycIn 21
Db 83327 TATCTTACCAGATTACCTATGATATACCGCTTGAGCGCTGTAATTTCTTGAA 83386
QY 22 Ile 22
Db 83387 ATT 83389

RESULT 33
US-10-156-761-5397
; Sequence 5397, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 5397
; LENGTH: 639
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; NAME/KEY: CDS
; LOCATION: (1)..(639)
US-10-156-761-5397

Alignment Scores:
Pred. No.: 0.00804 Length: 639
Score: 68.00 Matches: 13
Percent Similarity: 73.08% Conservative: 6
Best Local Similarity: 50.00% Mismatches: 7
Query Match: 46.90% Indels: 0
DB: 15 Gaps: 0

US-09-987-190-2 (1-30) x US-10-156-761-5397 (1-639)

QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlycIn 21
Db 10 TACACACTCCCGAAGTCCGCTACGACTCTCCGCGCTCGCCCGCTGATCAGCCCCGAG 69
QY 22 IleAsnGluIle**Tyr 27
Db 70 ATCATGAGAGCTGCACACCAC 87

RESULT 34
```

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US-10-297-465A-1/c
; Sequence 1, Application US/10297465A
; Publication No. US20040142413A1
; GENERAL INFORMATION:
; APPLICANT: Simpson, Andrew
; APPLICANT: Reinach, Fernando
; APPLICANT: Secubal, Joao
; APPLICANT: Mediantis, Joao
; APPLICANT: Arruda, Paulo
; TITLE OF INVENTION: Isolated Genome of Xylella fastidiosa and Uses Thereof
; FILE REFERENCE: FAPESP 202 US (10213376)
; CURRENT APPLICATION NUMBER: US/10/297,465A
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: PCT/IB01/01618
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,906
; PRIOR FILING DATE: 2001-06-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 2731748
; TYPE: DNA
; ORGANISM: Xylella fastidiosa
US-10-297-465A-1

Alignment Scores:
Pred. No.: 418 Length: 2731748
Score: 68.00 Matches: 13
Percent Similarity: 62.96% Conservative: 4
Best Local Similarity: 48.15% Mismatches: 10
Query Match: 46.90% Indels: 0
DB: 17 Gaps: 0

US-09-987-190-2 (1-30) x US-10-297-465A-1 (1-2731748)

QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlycIn 21
Db 2495021 TACACCTTCCCACTCTGCTTACGCTTACGATGCGTTCGACCGCATTTGATGCGCAG 2494962
QY 22 IleAsnGluIle**TyrThr 28
Db 2494961 ACAATGAAATCCATTACACC 2494941

RESULT 35
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
```

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Alignment Scores:
Pred. No.: 1.97e+03 Length: 9025608
Score: 68.00 Matches: 13
Percent Similarity: 73.08% Conservative: 6
Best Local Similarity: 50.00% Mismatches: 7
Query Match: 46.90% Indels: 0
DB: 15 Gaps: 0

US-09-987-190-2 (1-30) x US-10-156-761-1 (1-9025608)
QY 2 TyrsrleuprogluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 6564056 TACACCTCCCTGACTGACTCCGCTGACTACTCCGCTGCGCCGCTGATCAGCCCCGAG 6563997
QY 22 Ileasngluile***Tyr 27
Db 6563996 ATCATCGAGCTGCACAC 6563979

RESULT 36
US-09-727-855B-6
; Sequence 6, Application US/09727855B
; Patent No. US20020168703A1
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFUL
; FILE REFERENCE: C38435/111694
; CURRENT APPLICATION NUMBER: US/09/727,855B
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Phaffia rhodozyma
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(594)
; OTHER INFORMATION:
US-09-727-855B-6

Alignment Scores:
Pred. No.: 0.0113 Length: 597
Score: 67.00 Matches: 12
Percent Similarity: 76.19% Conservative: 4
Best Local Similarity: 57.14% Mismatches: 5
Query Match: 46.21% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x US-09-727-855B-6 (1-597)
QY 2 TyrsrleuprogluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 10 TACACCTCCCTGACTGACTCCGCTGACTACTCCGCTGCGCCGCTGATCAGCCCCGAG 69
QY 22 Ile 22
Db 70 ATC 72

RESULT 37
US-10-310-154-294
; Sequence 294, Application US/10310154
; Publication No. US2003023670A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Chomet, Paul S.
; APPLICANT: Adams, Thomas H
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Agarwal, Ameet K.
; APPLICANT: Ahrens, Jeffrey E.
```

```
; APPLICANT: Ball, James A.
; APPLICANT: Banu, G.
; APPLICANT: Bell, Erin
; APPLICANT: Boddapalli, Raghava
; APPLICANT: Delkman, Jili
; APPLICANT: Deng, Molian
; APPLICANT: Dong, Jinzhuo
; APPLICANT: Duff, Stephen M.
; APPLICANT: Galligan, Meghan M.
; APPLICANT: Hinchey, Brenda S.
; APPLICANT: Huang, Shishieh
; APPLICANT: Johnson, G. Richard
; APPLICANT: Jung, Vincent
; APPLICANT: Kretzmer, Keith A.
; APPLICANT: Laccetti, Lucille B.
; APPLICANT: Lai, Chao-Qiang
; APPLICANT: Lee, Gary
; APPLICANT: Lin, Jie-Yi
; APPLICANT: Liu, Jindong
; APPLICANT: Lu, Bin
; APPLICANT: Luethy, Michael M.
; APPLICANT: Lund, Adrian
; APPLICANT: Madson, Linda L.
; APPLICANT: Mallory, Kathleen A.
; APPLICANT: McKiel, Christine L.
; APPLICANT: Miller, Philip W.
; APPLICANT: Padmavathi, Manohikanti
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Start, William G.
; APPLICANT: Temmesen, Dan
; APPLICANT: Vidya, K.R.
; APPLICANT: Wang, Haiyun
; APPLICANT: Xin, Zhanqiao
; APPLICANT: Xu, Nanfei
; APPLICANT: Yang, Chunzhi
; APPLICANT: Zeng, Xiaoping
; APPLICANT: Zhang, Qiang
; APPLICANT: Zhou, Li
; TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
; FILE REFERENCE: 38-15 (52796)B
; CURRENT APPLICATION NUMBER: US/10/310,154
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,358
; NUMBER OF SEQ ID NOS: 736
; SEQ ID NO 294
; LENGTH: 1295
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (249)..(947)
; OTHER INFORMATION:
US-10-310-154-294

Alignment Scores:
Pred. No.: 0.0309 Length: 1295
Score: 67.00 Matches: 12
Percent Similarity: 72.00% Conservative: 6
Best Local Similarity: 48.00% Mismatches: 7
Query Match: 46.21% Indels: 0
DB: 16 Gaps: 0

US-09-987-190-2 (1-30) x US-10-310-154-294 (1-1295)
QY 3 SerleuprogluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 22
Db 348 GCGCTCCCGACCTCTCTTACGACTCGCGCTGAGCGCGCCATCTCGGGAGATC 407
QY 23 Asngluile***Tyr 27
Db 408 ATGCGCTGCACAC 422
```

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RESULT 38
US-10-329-960-1/C
; Sequence 1, Application US/10329960
; Publication No. US2003009277A1
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Frag
; TITLE OF INVENTION: Thereof, and Uses Thereof
; FILE REFERENCE: PB186P1
; CURRENT APPLICATION NUMBER: US/10/329,960
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: US 09/643,990
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 08/487,429
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/426,787
; PRIOR FILING DATE: 1995-04-21
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1830121
; TYPE: DNA
; ORGANISM: Haemophilus influenzae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4747)..(4747)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9921)..(9921)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10150)..(10150)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (29298)..(29298)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (36543)..(36543)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (36551)..(36551)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (36636)..(36636)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (40808)..(40810)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (44416)..(44416)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (44905)..(44905)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (44975)..(44975)
; OTHER INFORMATION: n equals a, t, g or c
; NAME/KEY: misc_feature
; LOCATION: (45593)..(45593)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
```

```
; NAME/KEY: misc_feature
; LOCATION: (45732)..(45732)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (47036)..(47036)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51334)..(51334)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51602)..(51602)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51786)..(51786)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51805)..(51805)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (55369)..(55369)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (65309)..(65309)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
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; NAME/KEY: misc_feature
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; FEATURE:
; NAME/KEY: misc_feature
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; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (117136)..(117136)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
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; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (119924)..(119924)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (120038)..(120038)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
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LOCATION:(121344)..(121344)
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OTHER INFORMATION: n equals a, t, g or c
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FEATURE:
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FEATURE:
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FEATURE:
NAME/KEY: misc_feature
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FEATURE:
NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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Alignment Scores:
Pred. No.: 381 Length: 1830121
Score: 67.00 Matches: 12
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 44.44% Mismatches: 9
Query Match: 46.21% Indels: 0
DB: 15 Gaps: 0

US-09-987-190-2 (1-30) x US-10-329-960-1 (1-1830121)

QY 2 TyriserleupProgiuleuaspTyrgiulubheseralatrrgiupProTyrlleserglgin 21
Db 1152886 TACAATCTCCCTGGAATTAGGCTATGCTACAAATGGCTAGAACACCAATTTGATGCGCA 1152822
QY 22 llaengluille**TyrThr 28

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Db      1152826 ACATGGAATCCATCATAGT 1152806
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RESULT 39
US-10-329-670-1/c
? Sequence 1, Application US/10329670
? Publication No. US20040018503A1
? GENERAL INFORMATION:
? APPLICANT: Fleischmann et al.
? TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Fragment
? FILE REFERENCE: PB186P1
? CURRENT APPLICATION NUMBER: US/10/329,670
? PRIORITY FILING DATE: 2002-12-24
? PRIOR APPLICATION NUMBER: US 09/643,990
? PRIOR FILING DATE: 2000-08-23
? PRIOR APPLICATION NUMBER: US 08/487,429
? PRIOR FILING DATE: 1995-06-07
? PRIOR APPLICATION NUMBER: US 08/426,787
? PRIOR FILING DATE: 1995-04-21
? NUMBER OF SEQ ID NOS: 1
? SOFTWARE: PatentIn version 3.1
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? FEATURE:
? NAME/KEY: misc_feature
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? NAME/KEY: misc_feature
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? NAME/KEY: misc_feature
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? FEATURE:
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (80024)..(80024)
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (100091)..(100091)
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FEATURE:
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LOCATION: (102696)..(102696)
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FEATURE:
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LOCATION: (105121)..(105121)
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FEATURE:
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LOCATION: (107248)..(107248)
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FEATURE:
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LOCATION: (117136)..(117136)
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (119750)..(119750)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (119924)..(119924)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (120038)..(120038)
OTHER INFORMATION: n equals a, t, g or c

```

```

FEATURE:
NAME/KEY: misc_feature
LOCATION: (121344)..(121344)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
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LOCATION: (122167)..(122167)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (122336)..(122336)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
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LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (131360)..(131360)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (139910)..(139910)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (140398)..(140398)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
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LOCATION: (142750)..(142750)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (145171)..(145171)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (145942)..(145942)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (147197)..(147197)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (152530)..(152530)

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Alignment Scores:

Pred. No.:	381	Length:	1830121
Score:	67.00	Matches:	12
Percent Similarity:	66.67%	Conservative:	6
Best Local Similarity:	44.44%	Mismatches:	9
Query Match:	46.21%	Indels:	0
DB:	16	Gaps:	0

US-09-987-190-2 (1-30) x US-10-329-670-1 (1-1830121)

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QY      2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaTrnGluProTyrIleSerGlyGln 21
Db      1152886 TACACTCTCCCTGATTAATGAGCTATGCTACATGCTTAGAACACCACTTTGATGCGCA 1152827

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QY 22 Ileasngluile***TyrThr 28

Db 1152826 ACAATGAAATCATCATAGT 1152806

RESULT 40

US-09-727-855B-4

/ Sequence 4, Application US/09727855B

/ Patent No. US20020168703A1

/ GENERAL INFORMATION:

/ APPLICANT: HOSHINO, Tatsuo

/ APPLICANT: OTIMA, Kazuyuki

/ APPLICANT: SETOGUCHI, Yutaka

/ TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOLIDS AND BIOLOGICALLY USEFUL

/ TITLE OF INVENTION: MATERIALS THEREOF

/ FILE REFERENCE: C38435/111694

/ CURRENT APPLICATION NUMBER: US/09/727,855B

/ CURRENT FILING DATE: 2000-12-01

/ NUMBER OF SEQ ID NOS: 17

/ SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 4

/ LENGTH: 669

/ TYPE: DNA

/ ORGANISM: Rhafilia rhodozyma

/ FEATURE:

/ NAME/KEY: CDS

/ LOCATION: (1)..(666)

/ OTHER INFORMATION: n or X = A, C, G or T

US-09-727-855B-4

Alignment Scores:

Pred. No.: 0.0201

Score: 66.00

Percent Similarity: 67.86%

Best Local Similarity: 46.43%

Query Match: 45.52%

DB: 9

Length: 669

Matches: 13

Conservative: 6

Mismatches: 9

Indels: 0

Gaps: 0

US-09-987-190-2 (1-30) x US-09-727-855B-4 (1-669)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

Db 76 AAGCATACCGCTGAGCTTCCTTACGATGCGCTGAGCCCTCCATCTCCAG 135

QY 21 GlnIleasngluile***TyrThr 28

Db 136 GAGATCATGACCTTCAACACACC 159

Search completed: September 1, 2004, 00:18:26
Job time : 4186 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 31, 2004, 11:39:57 ; Search time 6688 Seconds

(without alignments)
133.951 Million cell updates/sec

SUMMARIES

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Title: US-09-987-190-2
Sequence: 1 KXSLPELDYERSATREPTISGQINEXITXX 30

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=x1h
-Q=/cgm2_1/USPTO.spool/US09987190/runat 24082004 161320 24742/app query fasta_1.199
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bites -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRR=US09987190.@CGN_1_1-3437.@runat 24082004 161320 24742 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

EST:*

1: em_estda:*

2: em_esthum:*

3: em_estlin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estrom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pin:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rtd:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

Result
No. Score Query
Match Length DB ID

Result No.	Score	Query Match Length DB ID	Description
1	141	97.2 862 29	CNS07DTU
2	92	63.4 519 28	A2929307
3	90	62.1 464 13	B0087025
4	87	60.0 379 14	CB935955
5	87	60.0 516 12	BP522973
6	84	57.9 493 13	B0061557
7	84	57.9 669 14	CD425832
8	84	57.9 746 13	B0060841
9	83	57.2 231 9	AT319465
10	83	57.2 265 9	AT320309
11	83	57.2 265 10	AW717655
12	83	57.2 267 9	AT318805
13	83	57.2 267 10	AW723904
14	83	57.2 269 9	AT321638
15	83	57.2 336 9	AT320505
16	83	57.2 339 9	AT318710
17	83	57.2 339 9	AT319577
18	83	57.2 340 10	AW715499
19	83	57.2 343 10	AW724497
20	83	57.2 401 10	AW724781
21	83	57.2 429 10	AW715120
22	83	57.2 429 10	AW715952
23	82	56.6 592 12	BT321452
24	82	56.6 689 12	BM266232
25	81	55.9 734 14	CD460741
26	80	55.2 241 11	AY246752
27	80	55.2 466 12	BM167690
28	80	55.2 580 14	CB686471
29	80	55.2 675 13	BX255380
30	80	55.2 682 14	CF883054
31	80	55.2 702 14	CF873019
32	80	55.2 758 14	CF903040
33	80	55.2 767 14	CF932896
34	80	55.2 828 14	CD467777
35	79	54.5 286 14	CA937400
36	79	54.5 306 10	AW733168
37	79	54.5 308 14	CA910188
38	79	54.5 419 12	BI498255
39	79	54.5 420 10	AW756619
40	79	54.5 425 10	BE210200
41	79	54.5 448 9	AI460811
42	79	54.5 448 9	AI460823
43	79	54.5 463 9	AW099772
44	79	54.5 470 12	BM892237
45	79	54.5 493 14	CA910190

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
T7 end of clone BDOA4015F01 of library BDOA from strain CBS 94 of
Candida tropicalis, genomic survey sequence.
ACCESSION
AL440909
VERSION
AL440909.1 GI:12224320
KEYWORDS
GSS.
SOURCE
Candida tropicalis
ORGANISM
Candida tropicalis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE
1 (bases 1 to 862)

AUTHORS Soucier, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brothier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durans, P., Lepingle, A., Llorente, B., Malbertuy, A., Neveglise, C., Ozier-Kalogeropoulos, O., Potter, S., Sautin, M., Tekala, F., Toffano-Nioche, C., Weslowski-Louvel, M., Wincker, P., and Weissbach, J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

JOURNAL FEMS Lett. 487 (1), 3-12 (2000)

MEDLINE 20584711

PUBMED 1152876

REFERENCE 2 (bases 1 to 862)

AUTHORS Blandin, G., Ozier-Kalogeropoulos, O., Wincker, P., Artiguenave, F., and Dujon, B.

TITLE Genomic exploration of the hemiascomycetous yeasts: 16. *Candida tropicalis*

JOURNAL FEMS Lett. 487 (1), 91-94 (2000)

MEDLINE 20584726

PUBMED 1152891

REFERENCE 3 (bases 1 to 862)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web: <http://www.genoscope.cns.fr>)

COMMENT This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *uvarum*, *Saccharomyces exiguus*, *Saccharomyces servazii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source

1..862

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/mol_type="genomic DNA"

/strain="CBS 94"

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/clone="BD0A015F01"

/clone_lib="BD0A"

/note="end : 77"

<124..>726

/note="similar to *Saccharomyces cerevisiae* ORF YHR008C [SOD2 ; superoxide dismutase (Mn) precursor, mitochondrial]

1"

/evidence=not_experimental

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Best Local Similarity:	96.43%	Mismatches:	1
Query Match:	97.24%	Indels:	0
DB:	29	Gaps:	0

US-09-987-190-2 (1-30) x CNS07DTU (1-862)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

DB 130 AAATATAGTTTACCGAATTGATGATTTTCTGCTACTGACCATATATTTCTGGA 189

QY 21 GlnIleAsnGluIle***TyrThr 28

DB 190 CAAATTAAATGAATTCATTACT 213

RESULT 2

LOCUS AZ929307

DEFINITION 479..dif24g04.s1 *Saccharomyces kluyveri* *Saccharomyces kluyveri*

ACCESSION AZ929307

VERSION AZ929307.1 GI:13500214

KEYWORDS GSS.

SOURCE *Saccharomyces kluyveri*

ORGANISM *Saccharomyces kluyveri*

REFERENCE 1 (bases 1 to 519)

AUTHORS Cliften, P.F., Hillier, L.W., Fulton, L., Graves, T., Miner, T., Gish, W.B., Waterston, R.H. and Johnston, M.

TITLE Surveying *Saccharomyces* genomes to identify functional elements by comparative DNA sequence analysis

JOURNAL Unpublished (2001)

COMMENT Contact: Johnston M

Department of Genetics

Washington University Medical School

Box 8232, 4566 Scott Ave., St. Louis, MO 63110, USA

Tel: 314 362 2735

Fax: 314 362 7855

Email: mj@genetics.wustl.edu

Class: random plasmid subclone.

FEATURES

source

1..519

/organism="Saccharomyces kluyveri"

/mol_type="genomic DNA"

/strain="NRRL Y-12651 (CBS 3082)"

/db_xref="taxon:4934"

/clone="479.dif24g04.s1"

/clone_lib="Saccharomyces kluyveri"

/note="Random genomic sequence"

ORIGIN

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Score:	92.00	Matches:	16
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Best Local Similarity:	57.14%	Mismatches:	5
Query Match:	63.45%	Indels:	0
DB:	28	Gaps:	0

US-09-987-190-2 (1-30) x AZ929307 (1-519)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

DB 371 AAGGTCACTTGCCAGACTTGACCTGCGACTTGGAACCCACATCTCGGGT 430

QY 21 GlnIleAsnGluIle***TyrThr 28

DB 431 CAAATCAACGAGTTGCACTACTCG 454

RESULT 3

LOCUS B0087025

DEFINITION 464 bp mRNA linear EST 05-APR-2002

CDNA Clone Crl_9_A14 5', mRNA sequence.

ACCESSION B0087025

VERSION B0087025.1 GI:20046226

KEYWORDS EST.

SOURCE Ceratopteris richardii

ORGANISM Ceratopteris richardii

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Moniliformophyes; Filicophyta; Filicopsida; Filicales; Pteridaceae; Ceratopteris.

REFERENCE 1 (bases 1 to 464)

AUTHORS Chatterjee, A., San Miguel, P., Stout, S.C., Banks, J. and Roux, S.J.

TITLE Expressed sequence tags of cDNA clones from a C. richardii library

JOURNAL Unpublished (2000)

COMMENT Contact: Roux SJ

Section of Molecular Cell and Developmental Biology

University of Texas

Biology Building, Room 16, Austin, TX 78712, USA

Tel: 512 471 4238

Fax: 512 232 3402
Email: sroux@uts.cc.utexas.edu
Plate: Cri_9 row: A column: 14
Seq primer: SP6.

FEATURES

source

Location/Qualifiers
1..464
/organism="Ceratopteris richardii"
/mol_type="mRNA"
/cultiVar="Brogn"
/db_xref="taxon:49495"
/clone="Cri_9_A14"
/tissue_type="Gametophyte"
/cell_type="Spore"
/dev_stage="20 hours after germination initiation"
/clone_lib="Ceratopteris Spore Library"
/note="Vector: pCMVSPORT6; EST sequence from cDNA library.
cDNA library constructed from mRNA isolated from C.
richardii spores that had developed for 20 hours after
their germination had been initiated by white light."

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	0.000101	464	16	1	0	0
Percent Similarity:	90.00					
Best Local Similarity:	81.48%					
Query Match:	59.26%					
DB:	62.07%					

US-09-987-190-2 (1-30) x B0087025 (1-464)

QY 2 TyTSerLeuProGluLeuApyTyTglnPhseRAlathrGluProTyTlleSerGlyGln 21

Db 154 TACTCTTTACCGAGCTAGCTAGATTATGAGCGCTTATGAGCGCTACATCAGTGGCGAA 213

QY 22 IleAsnGluIle***TyrThr 28

Db 214 ATTATGAGCTGCATCATCAGC 234

RESULT 4

CB935955

LOCUS

CB935955 379 bp mRNA linear EST 29-APR-2003
taaa2a04.y2 Hydra EST -111 Hydra magnipapillata cDNA 5' similar to
SM:SODM_HUMAN P04179 SUPEROXIDE DISMUTASE [NM], MITOCHONDRIAL
PRECURSOR, mRNA sequence.

ACCESSION

CB935955 GI:30221346

VERSION

Hydra magnipapillata

KEYWORDS

EST.

SOURCE

Hydra magnipapillata

ORGANISM

Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Anthomedusae;

REFERENCE

Hydridae; Hydra.

AUTHORS

1 (bases 1 to 379)

TITLE

Bode,H., Blumberg,B., Steele,R., Widge,P., Gee,L., Nguyen,Q.,

JOURNAL

Martinez,D., Kibler,D., Hampton,S., Clifton,S., Pape,D., Barra,M.,

COMMENT

Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y.,

Gibbons,M., Rutter,B., Bennett,J., Ronko,I., Tsagarelisvilli,R.,

Maguire,L., Kennedy,S., Waterston,R. and Wilson,R.

WashU Hydra EST Project

Unpublished (2002)

Contact: Hans Bode

WashU Hydra EST Project

Washington University School of Medicine

444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Library was constructed by Bruce Blumberg & Jisong Pang, Univ. of

Calif. Irvine. Library materials provided by Hans Bode & Lydia Gee,

Univ. of Calif., Irvine. DNA sequencing by: Washington University

Genome Sequencing Center For information on obtaining a clone

please contact: Hans Bode (hrobod@uci.edu)

Trace considered overall poor quality

Seq primer: -40RP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..379

FEATURES

source

/organism="Hydra magnipapillata"
/mol_type="mRNA"
/db_xref="taxon:6085"
/lab_host="DH10B"
/clone_lib="Hydra EST -111"
/note="Vector: pCS22; Site 1: XhoI; Site 2: PstI; a) 1st
strand cDNA was primed with a XhoI oligo (dT) primer (5'
ACTAAGAGGCTCGAG(T)18NN) 3'; b) Double-stranded cDNA was
ligated to PstI linker, digested with PstI and XhoI and
cloned into the PstI and XhoI sites of a pCS22 vector,
which is a modified pCS2+ vector. c) The pCS22 vector
contains a T7 promoter site [standard from pluescript] at
the 5' end of the cloning site, and a T3 promoter site
[standard from pluescript] at the 3' end of the cloning
site. d) The ligation mix was transformed into TOP10P
cells (= DH10B cells). e) The cells were grown in SOC =
5% yeast, 20% tryptone, 0.5% NaCl, 10mM MgSO4, 10mM MgCl,
0.2% glucose/liter, (no antibiotic). f) The frequency of
vectors containing inserts is >90% [42 of 42]. g) The
average size of the 42 inserts is 1075 +/- 8501."

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	0.000242	379	17	5	0	0
Percent Similarity:	87.00					
Best Local Similarity:	81.48%					
Query Match:	62.96%					
DB:	60.00%					

US-09-987-190-2 (1-30) x CB935955 (1-379)

QY 1 TyTSerLeuProGluLeuApyTyTglnPhseRAlathrGluProTyTlleSerGly 20

Db 5 AAGCACACTCTTCCAGAAATTGGGCTATGATTAATGATTCATGTGACCAACCAATCAGCGGT 64

QY 21 GlnIleAsnGluIle***Tyr 27

Db 65 CAAATATGAGATCATCATCAT 85

RESULT 5

BP522973

LOCUS

BP522973 516 bp mRNA linear EST 17-SEP-2003
BP522973 Hydra magnipapillata cDNA library Hydra magnipapillata
cDNA clone hmp_21051, mRNA sequence.

ACCESSION

BP522973 GI:34829671

VERSION

EST.

KEYWORDS

Hydra magnipapillata

SOURCE

Hydra magnipapillata

ORGANISM

Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Anthomedusae;

REFERENCE

Hydridae; Hydra.

AUTHORS

1 (bases 1 to 516)

TITLE

Hayakawa,S., Hwang,U.S., Nishimiya-Fujisawa,C., Ogura,A., Ikeo,K.,

JOURNAL

Fujisawa,T. and Gotohori,T.

COMMENT

Hydra EST project

Unpublished (2003)

Contact: Jung Shan Hwang

Center for Information Biology and DNA Data Bank of Japan

National Institute of Genetics

111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-55-981-6847 (ex. 6898)

Fax: 81-55-981-6848

Email: jshwang@lab.nig.ac.jp, URL: http://www.cdb.nig.ac.jp.

Location/Qualifiers
1..516
/organism="Hydra magnipapillata"
/mol_type="mRNA"
/strain="105"

/db_xref="taxon:6085"
 /clone="hmp.21051"
 /tissue_type="whole body"
 /dev_stage="adult budding stage"
 /clone_lib="Hydra magnipapillata cDNA library"

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Score:
0.000362	516	17	87.00
Percent Similarity:		Conservative:	81.48%
Best Local Similarity:		Mismatches:	62.96%
Query Match:		Indels:	60.00%
DB:	12	Gaps:	0

US-09-987-190-2 (1-30) x BP522973 (1-516)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

Db 110 AAGCACCTCTCCAGATTGGGCTATGAATATATCATCTGGACCAACATCAGCGT 169

QY 21 GlnIleAsnGluIle***Tyr 27

Db 170 CAATTATGAGATATCATCAT 190

RESULT 6 BU061557 493 bp mRNA linear EST 26-AUG-2002

LOCUS Fgt.10.E01_T3 Nitrogen-starved mycelia Gibberella zeae cDNA, mRNA

DEFINITION BU061557

ACCESSION BU061557.1 GI:22501846

VERSION EST.

KEYWORDS Gibberella zeae

SOURCE Gibberella zeae

ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

REFERENCE 1 (bases 1 to 493)

AUTHORS Trail,F., Xu,J.-R., San Miguel,P., Halgren,R.G. and Kistler,H.C.

TITLE Analysis of expressed sequence tags from Gibberella zeae (anamorph

Fusarium graminearum)

JOURNAL Fungal Genet. Biol. 38 (2), 187-197 (2003)

MEDLINE 22508120

COMMENT Contact: Frances Trail

Department of Plant Biology

Michigan State University

East Lansing, MI 48824, USA

Tel: 517 432 2939

Fax: 517 353 1926

Email: trail@msu.edu

Plate: 10 row: E column: 01.

Location/Qualifiers

1..493

/organism="Gibberella zeae"

/mol_type="mRNA"

/strain="NRRL 31084"

/db_xref="taxon:5518"

/clone_lib="Nitrogen-starved mycelia"

/note="Vector: Uni-ZapII; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Score:
0.00107	493	15	84.00
Percent Similarity:		Conservative:	78.57%
Best Local Similarity:		Mismatches:	53.57%
Query Match:		Indels:	57.93%
DB:	13	Gaps:	0

US-09-987-190-2 (1-30) x BU061557 (1-493)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

Db 123 AAGGCACCTCTCCCGATCTTCCACGATAGATGCGCTTGTAGCCCTCATCTCTGAC 182

QY 21 GlnIleAsnGluIle***Tyr-Thr 28

Db 183 CAGATCATGAGCTTCACCACTCC 206

RESULT 7 CD425832 669 bp mRNA linear EST 02-JUN-2003

LOCUS SAI_14.C11.g1.A002 Salicylic acid-treated seedlings Sorghum bicolor

DEFINITION CDNA clone SAI_14.C11.A002 5', mRNA sequence.

ACCESSION CD425832

VERSION CD425832.1 GI:31332095

KEYWORDS EST.

SOURCE Sorghum bicolor (sorghum)

ORGANISM Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoidae; Andropogoneae; Sorghum.

1 (bases 1 to 669)

Cordonnier-Pratt,M.-M., Wentzel,V., Suzuki,Y., Sugano,S.,

Klein,R.R., Liang,C., Sun,F., Sullivan,R., Shah,M., Salzman,R.,

Chua Tan,N., Gonzalez,M., Lane,S., Miller,V., Nanda,P.,

Olaseinde,O., Eastman,A. and Pratt,L.H.

An EST database from Sorghum: salicylic acid-treated seedlings

Unpublished (2003)

Other ESTs: SAI_14.C11.B1.A002

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmp@prattengr.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in

the Human Genome Center, University of Tokyo. Institute of Medical

science; plant material and RNA prepared at Texas A & M University;

sequencing done in the Laboratory for Genomics and Bioinformatics;

University of Georgia. Sequence ends have been trimmed to exclude

vector and regions below Phred quality 16. Three-prime sequences

are presented as their reverse complement and have been trimmed to

exclude polyA.

Seq primer: Sug5 (CTTCTGCTTAAAGCTGCG).

FEATURES

Source

1..669

/organism="Sorghum bicolor"

/mol_type="mRNA"

/cultivar="Brx623"

/db_xref="taxon:4558"

/clone="SAI_14.C11.A002"

/lab_host="DH10B-TI phage-resistant E. coli"

/clone_lib="salicylic acid-treated seedlings"

/note="Vector: pME18S-Fl3; Site_1: XhoI; Site_2: XhoI; The

library was prepared from polyA+ RNA from seedlings grown

in hydroponic culture. At 8 days of age, medium was

supplemented with 1 mM salicylic acid (SA). Roots and

shoots were harvested after 27 and 72 hr and material from

both time points was combined prior to RNA isolation.

Double-stranded cDNA was cloned unidirectionally into

different DraIII sites of the pME18S-Fl3 vector (5-prime

DraIII site is CACTGTGT, 3-prime DraIII site is

CACCATGTG). XhoI excises the cDNA insert."

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Score:
0.00159	669	15	84.00
Percent Similarity:		Conservative:	78.57%
Best Local Similarity:		Mismatches:	53.57%
Query Match:		Indels:	57.93%
DB:	14	Gaps:	0

US-09-987-190-2 (1-30) x CD425832 (1-669)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 Db 299 AAGGCCACCTCCCGGACCTTCCTACGATATGAGCGCTCTTGAGCCCTACATCTCCGCG 358
 QY 21 GlnIleAsnGluIle***TyrThr 28
 Db 359 CAGATCATGAGGCTTCACCACTCC 382

RESULT 8
 BU060841 746 bp mRNA linear EST 26-AUG-2002
 LOCUS BU060841
 DEFINITION Fgr-C_1.K18_T3 Carbon-starved mycelia Gibberella zeae cDNA, mRNA
 sequence.
 ACCESSION BU060841 GI:22501130
 VERSION BU060841.1
 KEYWORDS EST.
 SOURCE Gibberella zeae
 ORGANISM Gibberella zeae

REFERENCE
 AUTHORS Bukarjota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
 TITLE Trail, F., Xu, J., R., San Miguel, P., Halgren, R.G. and Kistler, H.C.
 Analysis of expressed sequence tags from Gibberella zeae (anamorph
 Fusarium graminearum)
 JOURNAL Fungal Genet. Biol. 38 (2), 187-197 (2003)
 MEDLINE 22508120
 PUBMED 12620255

COMMENT
 Contact: Frances Trail
 Department of Plant Biology
 Michigan State University
 East Lansing, MI 48824, USA
 Tel: 517 432 2939
 Fax: 517 353 1926
 Email: trail@msu.edu
 Plate: 1 row: K column: 18.

FEATURES
 source
 Location/Qualifiers
 1..746
 /organism="Gibberella zeae"
 /mol_type="mRNA"
 /strain="NRRL 31084"
 /db_xref="taxon:5518"
 /clone_lib="Carbon-starved mycelia"
 /note="Vector: Uni-ZapII; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
 Alignment Scores:
 Pred. No.: 0.00183 Length: 746
 Score: 84.00 Matches: 15
 Percent Similarity: 78.57% Conservative: 7
 Best Local Similarity: 53.57% Mismatches: 6
 Query Match: 57.93% Indels: 0
 DB: 13 Gaps: 0

US-09-987-190-2 (1-30) x BU060841 (1-746)
 QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 Db 134 AAGGCCACCTCCCGGACCTTCCTACGATATGAGCGCTCTTGAGCCCTACATCTCTGCG 193
 QY 21 GlnIleAsnGluIle***TyrThr 28
 Db 194 CAGATCATGAGGCTTCACCACTCC 217

RESULT 9
 AI319465 231 bp mRNA linear EST 18-DEC-1998
 LOCUS AI319465
 DEFINITION b2a04nm.f1 Neurospora crassa morning cDNA library Neurospora crassa
 cDNA clone b2a04nm 5', mRNA sequence.
 ACCESSION AI319465
 VERSION AI319465.1 GI:4035447
 KEYWORDS EST.

SOURCE

Neurospora crassa

Neurospora crassa

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

REFERENCE

1 (bases 1 to 231)
 Zhu, H., Lai, H., Kupfer, D., Dunlap, J.C. and Roe, B.A.

AUTHORS

Two Neurospora crassa EST Databases
 Unpublished (1998)

Contact: Bruce A. Roe, University of Oklahoma, broeou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broeou.edu

We anticipate the future release of the cDNA clones to the Fungal
 Genetics Stock Center
 Seq primer: Universal Forward Primer
 High quality sequence stop: 50.

FEATURES

source

Location/Qualifiers
 1..231
 /organism="Neurospora crassa"
 /mol_type="mRNA"
 /strain="bd, frg7 A"
 /db_xref="taxon:5141"
 /clone="b2a04nm"
 /tissue_type="tissue harvested following 22hr growth in
 dark"
 /clone_lib="Neurospora crassa morning cDNA library"
 /note="Vector: pBluescript SK-; Site 1: XbaI; Site 2:
 EcoRI; See: Bell-Pedersen, D., et al. PNAS 93:13096-1996.
 5' end of cDNA cloned into XbaI site of pBluescript, 3'
 end of cDNA cloned into EcoRI site of pBluescript"

ORIGIN

Alignment Scores:

Pred. No.: 0.000585 Length: 231
 Score: 83.00 Matches: 15
 Percent Similarity: 77.78% Conservative: 6
 Best Local Similarity: 55.56% Mismatches: 6
 Query Match: 57.24% Indels: 0
 DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x AI319465 (1-231)

QY 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 21
 Db 65 TATTCCTCCGACGCTACCATATGCTCAATGCTGAGCCCTACATCTCAGCCGAG 124

QY 22 IleAsnGluIle***TyrThr 28
 Db 125 ATCATGAGGCTTCACCAAGC 145

RESULT 10

AI320309 265 bp mRNA linear EST 18-DEC-1998
 LOCUS AI320309
 DEFINITION c3b05nm.f1 Neurospora crassa morning cDNA library Neurospora crassa
 cDNA clone c3b05nm 5', mRNA sequence.
 ACCESSION AI320309
 VERSION AI320309.1 GI:4036291

KEYWORDS

SOURCE

ORGANISM

Neurospora crassa

Neurospora crassa

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

REFERENCE

1 (bases 1 to 265)
 Zhu, H., Lai, H., Kupfer, D., Dunlap, J.C. and Roe, B.A.

AUTHORS

Two Neurospora crassa EST Databases
 Unpublished (1998)

JOURNAL

Other ESTs: c3b05nm.f1

Contact: Bruce A. Roe, University of Oklahoma, broeou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma


```

VERSION      AI320505.1  GI:4036487
KEYWORDS     EST.
SOURCE       Neurospora crassa
ORGANISM     Neurospora crassa
             Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
             Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE    1 (bases 1 to 336)
TITLE        Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
JOURNAL      Two Neurospora crassa EST Databases
COMMENT      Unpublished (1998)
             Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
             Department of Chemistry and Biochemistry
             Advanced Center for Genome Technology, University of Oklahoma
             620 Parrington Oval, Norman, OK 73019, USA
             Tel: 405 325 4912
             Fax: 405 325 7762
             Email: broe@ou.edu
             We anticipate the future release of the cDNA clones to the Fungal
             Genetics Stock Center
             Seq primer: Universal Forward Primer
             High quality sequence stop: 194.
             Location/Qualifiers
               1..336
               /organism="Neurospora crassa"
               /mol_type="mRNA"
               /strain="bd, frq7 A"
               /db_xref="taxon:5141"
               /clone="csh03nm"
               /tissue_type="tissue harvested following 22hr growth in
               dark"
               /clone_1lb="Neurospora crassa morning cDNA library"
               /note="Vector: pBluescript SK-; Site 1: XbaI; Site 2:
               EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
               5' end of cDNA cloned into XbaI site of pBluescript; 3'
               end of cDNA cloned into EcoRI site of pBluescript"

ORIGIN
Alignment Scores:
Pred. No.:      0.000951      Length:      336
Score:          83.00         Matches:      15
Percent Similarity: 77.78%    Conservative: 6
Best Local Similarity: 55.56% Mismatches:      6
Query Match:    57.24%       Indels:         0
DB:             9            Gaps:          0

US-09-987-190-2 (1-30) x AI320505 (1-336)
QY      2 TTTCTCTCTCCGAGCTTACCATATGCTGAGAGCCCTACATCTCAGCCGAG 124
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
        65 TATTCCTTCCGAGCTTACCATATGCTGAGAGCCCTACATCTCAGCCGAG 124
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY      22 TleAsnGluIle***TyrThr 28
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
        125 ATCATGAGGCTTACCATCAGC 145
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 16
LOCUS       AI318710      339 bp      mRNA      linear      EST 18-DEC-1998
DEFINITION albl0nm.f1 Neurospora crassa morning cDNA library Neurospora crassa
            cDNA clone albl0nm 5', mRNA sequence.
ACCESSION   AI318710
VERSION     AI318710.1  GI:4034645
KEYWORDS    RST.
SOURCE      Neurospora crassa
ORGANISM    Neurospora crassa
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE    1 (bases 1 to 339)
TITLE        Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
JOURNAL      Two Neurospora crassa EST Databases
COMMENT      Unpublished (1998)
             Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
             Department of Chemistry and Biochemistry

```

```

Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seq primer: Universal Forward Primer
High quality sequence stop: 309.
Location/Qualifiers
  1..339
  /organism="Neurospora crassa"
  /mol_type="mRNA"
  /strain="bd, frq7 A"
  /db_xref="taxon:5141"
  /clone="albl0nm"
  /tissue_type="tissue harvested following 22hr growth in
  dark"
  /clone_1lb="Neurospora crassa morning cDNA library"
  /note="Vector: pBluescript SK-; Site 1: XbaI; Site 2:
  EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
  5' end of cDNA cloned into XbaI site of pBluescript; 3'
  end of cDNA cloned into EcoRI site of pBluescript"

ORIGIN
Alignment Scores:
Pred. No.:      0.000962      Length:      339
Score:          83.00         Matches:      15
Percent Similarity: 77.78%    Conservative: 6
Best Local Similarity: 55.56% Mismatches:      6
Query Match:    57.24%       Indels:         0
DB:             9            Gaps:          0

US-09-987-190-2 (1-30) x AI318710 (1-339)
QY      2 TTTCTCTCTCCGAGCTTACCATATGCTGAGAGCCCTACATCTCAGCCGAG 124
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
        65 TATTCCTTCCGAGCTTACCATATGCTGAGAGCCCTACATCTCAGCCGAG 124
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
        :|:|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~
QY      22 TleAsnGluIle***TyrThr 28
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
        :|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~
        125 ATCATGAGGCTTACCATCAGC 145
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
        :|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~

RESULT 17
LOCUS       AI319577      339 bp      mRNA      linear      EST 18-DEC-1998
DEFINITION b3g06nm.f1 Neurospora crassa morning cDNA library Neurospora crassa
            cDNA clone b3g06nm 5', mRNA sequence.
ACCESSION   AI319577
VERSION     AI319577.1  GI:4035559
KEYWORDS    EST.
SOURCE      Neurospora crassa
ORGANISM    Neurospora crassa
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE    1 (bases 1 to 339)
TITLE        Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
JOURNAL      Two Neurospora crassa EST Databases
COMMENT      Unpublished (1998)
             Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
             Department of Chemistry and Biochemistry
             Advanced Center for Genome Technology, University of Oklahoma
             620 Parrington Oval, Norman, OK 73019, USA
             Tel: 405 325 4912
             Fax: 405 325 7762
             Email: broe@ou.edu
             We anticipate the future release of the cDNA clones to the Fungal
             Genetics Stock Center
             Seq primer: Universal Forward Primer
             High quality sequence stop: 314.
             Location/Qualifiers
               1..339
               /organism="Neurospora crassa"

```

ORIGIN

Alignment Scores:
Pred. No.: 0.000962 Length: 339
Score: 83.00 Matches: 15
Percent Similarity: 77.78% Conservative: 6
Best Local Similarity: 55.56% Mismatches: 6
Query Match: 57.24% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x A1319577 (1-339)

QY 2 TysSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
|||||
Db 65 TATTCCTTCGCGAGCTACCATATGCTCAATGCTGTGGAGCCCTACATCTCAGCCGAG 124
|||||
QY 22 IleAsnGluIle***TyrThr 28
|||||
Db 125 ATCATGAGCTTCACCCAGC 145
|||||

RESULT 18
AW715499 340 bp mRNA linear EST 19-APR-2000
LOCUS g4f03nm.f1 Neurospora crassa morning CDNA library Neurospora crassa
DEFINITION cDNA clone g4f03nm 5', mRNA sequence.
ACCESSION AW715499
VERSION AW715499.1 GI:7604640
KEYWORDS EST.
SOURCE Neurospora crassa
ORGANISM Neurospora crassa

REFERENCE
1 (bases 1 to 340)
Sordariomyces, Sordariaceae, Sordariomycetes;
Zhu, H., Lai, H., Kupfer, D., Dunlap, J.C. and Roe, B.A.
TWO Neurospora crassa EST Databases
Unpublished (1998)
CONTACT: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu

FEATURES
source
We anticipate the future release of the CDNA clones to the Fungal
Seq primer: Universal Forward Primer
High quality sequence stop: 315.
Location/Qualifiers
1..340

/organism="Neurospora crassa"

/mol_type="mRNA"

/strain="bd, frq7 A"

/db_xref="taxon:5141"

/clone="g4f03nm"

/tissue_type="tissue harvested following 22hr growth in dark"

/clone_lib="Neurospora crassa morning CDNA library"

/note="Vector: pBluescript SK-; Site 1: XbaI; Site 2: EcoRI; See: Bell-Pedersen, D., et al. PNAS 93:13096,1996.

5' end of CDNA cloned into XbaI site of pBluescript; 3'

end of CDNA cloned into EcoRI site of pBluescript"

ORIGIN

Alignment Scores:

Pred. No.: 0.000966 Length: 340
Score: 83.00 Matches: 15
Percent Similarity: 77.78% Conservative: 6
Best Local Similarity: 55.56% Mismatches: 6
Query Match: 57.24% Indels: 0
DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x AW715499 (1-340)

QY 2 TysSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
|||||
Db 65 TATTCCTTCGCGAGCTACCATATGCTCAATGCTGTGGAGCCCTACATCTCAGCCGAG 124
|||||
QY 22 IleAsnGluIle***TyrThr 28
|||||
Db 125 ATCATGAGCTTCACCCAGC 145
|||||

RESULT 19
AW724497 343 bp mRNA linear EST 19-APR-2000
LOCUS f6b04nm.f1 Neurospora crassa morning CDNA library Neurospora crassa
DEFINITION cDNA clone f6b04nm 5', mRNA sequence.
ACCESSION AW724497
VERSION AW724497.1 GI:7619057
KEYWORDS EST.
SOURCE Neurospora crassa
ORGANISM Neurospora crassa

REFERENCE
1 (bases 1 to 343)
Sordariomyces, Sordariaceae, Sordariomycetes;
Zhu, H., Lai, H., Kupfer, D., Dunlap, J.C. and Roe, B.A.
TWO Neurospora crassa EST Databases
Unpublished (1998)
CONTACT: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu

FEATURES
source
We anticipate the future release of the CDNA clones to the Fungal
Seq primer: Universal Forward Primer
High quality sequence stop: 324.
Location/Qualifiers
1..343

/organism="Neurospora crassa"

/mol_type="mRNA"

/strain="bd, frq7 A"

/db_xref="taxon:5141"

/clone="f6b04nm"

/tissue_type="tissue harvested following 22hr growth in dark"

/clone_lib="Neurospora crassa morning CDNA library"

/note="Vector: pBluescript SK-; Site 1: XbaI; Site 2: EcoRI; See: Bell-Pedersen, D., et al. PNAS 93:13096,1996.

5' end of CDNA cloned into XbaI site of pBluescript; 3'

end of CDNA cloned into EcoRI site of pBluescript"

ORIGIN

Alignment Scores:

Pred. No.: 0.000977 Length: 343
Score: 83.00 Matches: 15
Percent Similarity: 77.78% Conservative: 6
Best Local Similarity: 55.56% Mismatches: 6
Query Match: 57.24% Indels: 0
DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x AW724497 (1-343)

QY 2 TysSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
|||||

```

Db      65 TATTCCTCCGAGCTACCATATGCTCATATGCTCTGAGCCCTACATCTCAGCCAG 124
QY      22 Tleasngluile***TyrThr 28
      125 ATCATGAGCTTCACACAGC 145

RESULT 20
AW724781
LOCUS   AW724781          401 bp    mRNA    linear    EST 19-APR-2000
DEFINITION   f8b07nm.f1 Neurospora crassa morning cDNA library Neurospora crassa
ACCESSION   AW724781
VERSION     AW724781
KEYWORDS    EST.
SOURCE      Neurospora crassa
ORGANISM    Neurospora crassa
REFERENCE   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
            1 (bases 1 to 401)
AUTHORS     Zhu, H., Lai, H., Kupfer, D., Dunlap, J.C. and Roe, B.A.
TITLES      Two Neurospora crassa EST Databases
JOURNAL     Unpublished (1998)
COMMENT     Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
            Department of Chemistry and Biochemistry
            Advanced Center for Genome Technology, University of Oklahoma
            620 Parrington Oval, Norman, OK 73019, USA
            Tel: 405 325 4912
            Fax: 405 325 7762
            Email: broe@ou.edu
            We anticipate the future release of the cDNA clones to the Fungal
            Genetics Stock Center
            Seq primer: Universal Forward Primer
            High quality sequence stop: 394.
            Location/Qualifiers
                1..401
                /organism="Neurospora crassa"
                /mol_type="mRNA"
                /strain="bd, frq7 A"
                /db_xref="taxon:5141"
                /clone="f8b07nm"
                /tissue_type="tissue harvested following 22hr growth in
                dark"
                /clone_1lb="Neurospora crassa morning cDNA library"
                /note="Vector: pBluescript SK-; Site 1: XbaI; Site 2:
                EcoRI; See: Bell-Pedersen, D., et al. FNAS 93:13096,1996.
                5' end of cDNA cloned into XbaI site of pBluescript; 3'
                end of cDNA cloned into EcoRI site of pBluescript."

ORIGIN
Alignment Scores:
Pred. No.:      0.0012      Length:      401
Score:          83.00      Matches:      15
Percent Similarity: 77.78%      Conservative: 6
Best Local Similarity: 55.56%      Mismatches: 6
Query Match:    57.24%      Indels:      0
DB:             10      Gaps:          0

US-09-987-190-2 (1-30) x AW724781 (1-401)

QY      2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
      65 TATTCCTCCGAGCTACCATATGCTCATATGCTCTGAGCCCTACATCTCAGCCAG 124
QY      22 Tleasngluile***TyrThr 28
      125 ATCATGAGCTTCACACAGC 145
Db

```

```

ACCESSION   AW715120
VERSION     AW715120.1 GI:7604309
KEYWORDS    EST.
SOURCE      Neurospora crassa
ORGANISM    Neurospora crassa
REFERENCE   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
            1 (bases 1 to 429)
AUTHORS     Zhu, H., Lai, H., Kupfer, D., Dunlap, J.C. and Roe, B.A.
TITLES      Two Neurospora crassa EST Databases
JOURNAL     Unpublished (1998)
COMMENT     Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
            Department of Chemistry and Biochemistry
            Advanced Center for Genome Technology, University of Oklahoma
            620 Parrington Oval, Norman, OK 73019, USA
            Tel: 405 325 4912
            Fax: 405 325 7762
            Email: broe@ou.edu
            We anticipate the future release of the cDNA clones to the Fungal
            Genetics Stock Center
            Seq primer: Universal Forward Primer
            High quality sequence stop: 336.
            Location/Qualifiers
                1..429
                /organism="Neurospora crassa"
                /mol_type="mRNA"
                /strain="bd, frq7 A"
                /db_xref="taxon:5141"
                /clone="g2c12nm"
                /tissue_type="tissue harvested following 22hr growth in
                dark"
                /clone_1lb="Neurospora crassa morning cDNA library"
                /note="Vector: pBluescript SK-; Site 1: XbaI; Site 2:
                EcoRI; See: Bell-Pedersen, D., et al. FNAS 93:13096,1996.
                5' end of cDNA cloned into XbaI site of pBluescript; 3'
                end of cDNA cloned into EcoRI site of pBluescript."

ORIGIN
Alignment Scores:
Pred. No.:      0.00131      Length:      429
Score:          83.00      Matches:      15
Percent Similarity: 77.78%      Conservative: 6
Best Local Similarity: 55.56%      Mismatches: 6
Query Match:    57.24%      Indels:      0
DB:             10      Gaps:          0

US-09-987-190-2 (1-30) x AW715120 (1-429)

QY      2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
      65 TATTCCTCCGAGCTACCATATGCTCATATGCTCTGAGCCCTACATCTCAGCCAG 124
QY      22 Tleasngluile***TyrThr 28
      125 ATCATGAGCTTCACACAGC 145
Db

```


COMMENT

Contact: Duplessis S
UMR 1136 INRA/UHP Interactions Arbres/Micro-Organismes
INRA
Centre INRA de Nancy, 54280 Champenoux, France
Tel.: + 33 383 39 40 13
Fax: + 33 383 39 40 69
Email: duplessis@nancy.inra.fr
Insert Length: 689 Std Error: 0.00
Seq primer: T3
POLYA=No.

FEATURES

Location/Qualifiers

1..689
/organism="Tuber borchii"
/mol_type="mRNA"
/db_xref="taxon:42251"
/tissue_type="mycelium"
/dev_stage="vegetative hyphae"
/clone_lib="cDNA library of Tuber borchii vegetative mycelium grown on PDA agar medium"
/note="Organ: mycelium; Vector: pBK-CMV phagemid; Site 1: EcoRI, Site 2: XhoI; The cDNA library was constructed from total RNA of Tuber borchii mycelium grown on PDA agar medium using the UniZapXR cDNA Library System Construction kit (Stratagene, USA) according to the manufacturer's instructions. UniZapXR clones were converted to pBK-CMV phagemid clones using E. coli BM25.8 as the bacterial host"

ORIGIN

Alignment Scores:

Pred. No.:	0.00353	Length:	689
Score:	82.00	Matches:	15
Percent Similarity:	75.00%	Conservative:	6
Best Local Similarity:	53.57%	Mismatches:	7
Query Match:	56.55%	Indels:	0
DB:	12	Gaps:	0

US-09-987-190-2 (1-30) x BM266232 (1-689)

QY

1 LysTySerLeuProGlnLeuAspTyrGlnPheSerAlaThrGluProTyrTrpSerGly 20
|||||::|||
Db 404 AAGTTACTCTTCGGCGATGCCGTAATCCTATGATGCCTGAACCTTACATCTCCGCGC 463
|||::|
QY 21 GlnIleAsnGluIle***TyrThr 28
|||::|
Db 464 CAAATTATGCACAATCACCAATTC 487
|||::|

RESULT 25

CD460741 734 bp mRNA linear EST 03-JUN-2003

LOCUS CD460741

DEFINITION Pg99_01k18_A Pg99 PAFC_ECORC_Fusarium graminearum simple_substrate

ACCESSION Gdbberella zeae cDNA clone Pg99_01k18, mRNA sequence.

VERSION CD460741

KEYWORDS CD460741.1 GI:31375481

SOURCE EST.

ORGANISM Gibberella zeae

REFERENCE Gibberella zeae
Eukaryota, Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
1 (bases 1 to 734)
Watson,R.J., Heyes,R., Coutoux,P., De Moors,A., Harris,L.J.,
Hatchori,J., Iacrotix,C., Maocuti,M., Ouellet,T., Robert,L.S.,
Singh,J.A., Spiroct,D. and Tinker,N.A.
A cDNA library prepared from Fusarium graminearum grown on a simple substrate

JOURNAL COMMENT Unpublished (2003)
Contact: Watson, Robert.J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
CANADA
Tel.: (613) 759-1655
Fax: (613) 759-1701

```

FEATURES
    source
        Email: watsouj@agr.gc.ca.
        Location/Qualifiers
            1..734
                /organism="Gibberella zeae"
                /mol_type="mRNA"
                /strain="DAOM 180378"
                /db_xref="taxon:5518"
                /clone="Pg09_01K18"
                /tissue_type="Mycelium"
                /dev_stage="asexual"
                /lab_host="E. coli DH10B"
                /clone_11b="Pg09_AAFc_ECORC_Fusarium_graminearum_simple_substrate"
                /notes="Vector: pBluescript II; Site 1: EcoRI; Site 2: XhoI; Fusarium graminearum grown on a simple substrate--minimal media supplemented with amino acids."

ORIGIN
Alignment Scores:
Pred. No.:      0.00561      Length:      734
Score:          81.00      Matches:      14
Percent Similarity: 80.00%      Conservative: 6
Best Local Similarity: 56.00%      Mismatches:  5
Query Match:      55.86%      Indels:      0
DB:              14      Gaps:      0

US-09-987-190-2 (1-30) x CD460741 (1-734)
QY      4  LeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGlnIleAsn 23
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      2  CTCCCGCATCTCCCTCCATGACATATGAGCGCTCTTGAGCCCTACATCTCGGCAGATCAKG 61
QY      24 GlnIle**TyrThr 28
        |||:::|:|||||:
Db      62 GAGCTTCACCACTCC 76

RESULT 26
AY246752      241 bp      mRNA      linear      HTC 01-SEP-2003
LOCUS      AY246752
DEFINITION      Equus caballus manganese superoxide dismutase (Mn-SOD) mRNA, 5' UTR
ACCESSION      AY246752
VERSION      AY246752.1 GI:32264465
KEYWORDS      HTC.
SOURCE      Equus caballus (horse)
ORGANISM      Equus caballus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE      1 (bases 1 to 241)
AUTHORS      Takafuji,Y.A., Crisman,M.V., Seat,K.L., Sharova,L.V., Ward,D.L. and Howard,R.D.
TITLE      Expression analysis of equine interleukin-1b treated equine synovium using suppression subtractive hybridization analysis (SSH-PCR)
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 241)
AUTHORS      Takafuji,Y.A., Crisman,M.V., Seat,K.L., Sharova,L.V. and Howard,R.D.
TITLE      Direct Submission
JOURNAL      Submitted (25-FEB-2003) VA-MD Regional College of Veterinary Medicine, Large Animal Clinical Sciences, Orthopedic Research Laboratory and Molecular Diagnostics Laboratory, Virginia Polytechnic Institute and State University, Duckpond Drive, Blacksburg, VA 24061, USA
FEATURES
    source
        Location/Qualifiers
            1..241
                /organism="Equus caballus"
                /mol_type="mRNA"
                /isolation_source="synovial tissue samples (1 gram) removed from middle carpal joint 6 hours following intrasynovial injection with recombinant equine interleukin-1b (100 ng)"
                /db_xref="taxon:9796"

```

ORIGIN	Alignment Scores:	Pred. No.:	0.00455	Length:	466
Score:	80.00	Matches:	15		
Percent Similarity:	76.92%	Conservative:	5		
Best Local Similarity:	57.69%	Mismatches:	6		
Query Match:	55.17%	Indels:	0		
DB:	12	Gaps:	0		
US-09-987-190-2 (1-30) x BM367690 (1-466)					
Qy	2 TySereIeufProgiIeueApTYrGluPheSerAlaThrGluProTYrIleSerGIyGln 21				
Db	204 TTGATGTTACCGGAGCTTCATACGAAATACAGCGCATTTGACACGGTTATTATGCGTACG 263				
Qy	22 TLeasnGluIeL***Tyr 27				
Db	264 ATTATGAGCCTTGACACGAC 281				
RESULT 28					
LOCUS	CB686471	580 bp	mRNA	linear	EST 04-SEP-2003
DEFINITION	CEST-01-B-09 Mixed source, strain EP15 and EP15 infected with hypovirus CHV1-EP713 Cryphonectria parasitica cDNA clone EP155, EP155-CHV1-EP713 5-prime, mRNA sequence.				
ACCESSION	CB686471				
VERSION	CB686471.1	GI:34447340			
KEYWORDS	EST.				
SOURCE	Cryphonectria parasitica				
ORGANISM	Cryphonectria parasitica				
	Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Diaporthales; Valsaceae; Cryphonectria-Endothia complex; Cryphonectria.				
REFERENCE	1 (bases 1 to 580)				
AUTHORS	Dawe,A.L., McMain,V.C., Panglao,M., Kasahara,S., Chen,B. and Nuss,D.L.				
TITLE	An ordered collection of expressed sequences from Cryphonectria parasitica and evidence of genomic microsynteny with Neurospora crassa and Magnaporthe grisea				
JOURNAL	Microbiology 149 (9), 2373-2384 (2003)				
MEDLINE	22830414				
PUBMED	12949163				
COMMENT	Contact: Dawe AL, Nuss DL Center for Biosystems Research University of Maryland Biotechnology Institute 5115 Plant Sciences Building, College Park, MD 20742, USA Tel: 301-405-7661 or 5111 Fax: 301-314-9075 Email: dawe@umbl.umd.edu Cryphonectria parasitica EST derived from mixed samples of cDNA from wild-type (strain EP155) and hypovirus-infected cultures. Seq primer: M13-reverse. Location/Qualifiers 1..580 /molecule="Cryphonectria parasitica" /mol_type="mRNA" /strain="EP155" /db_xref="taxon:5116" /db_xref="ATCC (inhost):38755 and 52571" /clone="EP155, EP155-CHV1-EP713" /clone_1b="Mixed source, strain EP155 and EP155 infected with hypovirus CHV1-EP713" /note="Cryphonectria parasitica EST derived from mixed samples of cDNA from wild-type (strain EP155) and hypovirus-infected cultures"				
FEATURES					
source					
ORIGIN					

Alignment Scores:

Pred. No.: 0.00605 Length: 580
 Score: 80.00 Matches: 14
 Percent Similarity: 78.57% Conservative: 8
 Best Local Similarity: 50.00% Mismatches: 6
 Query Match: 55.17% Indels: 0
 DB: 14 Gaps: 0

US-09-987-190-2 (1-30) x CB686471 (1-580)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 20

Db 181 AAGGCTACTCTACCAAGACTCTCCCTGACTAGACGGCGCCCTGAACTCACAATCTCGGAC 240

QY 21 GlnIleAsnGluIle**TyrThr 28

Db 241 CAGATCATGAGCTCCACCAATTC 264

RESULT 29

LOCUS BX255380 675 bp mRNA linear EST 25-FEB-2003

DEFINITION BX255380 Pinus pinaster differentiating xylem adult Pinus pinaster

ACCESSION CDNA clone PP005B07, mRNA sequence.

VERSION BX255380

KEYWORDS EST

SOURCE Pinus pinaster

ORGANISM Pinus pinaster

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

1 (bases 1 to 675)

Darvaz, A., Fereira, P., Avila, C., Mouret, J.-F., Brach, J., de

Transcriptome analysis of wood formation in maritime pine

Unpublished (2003)

Contact: Frigerio JM

Genetique et Amelioration 69

INRA

Route d'Arcachon 33612 Cestas CEDEX France

Email: Frigerio@pierrotton.inra.fr

Email: Frigerio@pierrotton.inra.fr

Location/Qualifiers

1 675

/organism="Pinus pinaster"

/mol_type="mRNA"

/strain="ecotype: Corsican"

/db_xref="taxon:71647"

/clone="PP005B07"

/rstage_type="differentiating xylem"

/dev_stage="adult"

/clone_lib="Pinus pinaster differentiating xylem adult"

/note="Vector: Uni-Zap XR lambda (Stratagene); Site 1: Eco

RI; Site 2: Xho I; A composite cDNA library was made with

mRNA isolated from normal, compression, opposite, early

and late wood of Maritime pine uni-directionally cloned

into uni-Zap XR using the Zap-cDNA Synthesis kit

(Stratagene). pluscript SK(-) plasmids were obtained by

in vivo mass excision. The nucleotide sequence of the

5' end was obtained by automated sequencing with the T3

primer by GENOME EXPRESS, Meylan, France"

ORIGIN

Alignment Scores:

Pred. No.: 0.00736 Length: 675

Score: 80.00 Matches: 15

Percent Similarity: 76.92% Conservative: 5

Best Local Similarity: 57.69% Mismatches: 6

Query Match: 55.17% Indels: 0

DB: 13 Gaps: 0

US-09-987-190-2 (1-30) x BX255380 (1-675)

QY 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 21

Db 215 TTGATTTACCGGAGCTTCCATACGATACAGTTCGATTCGAAACCGCTTATTAGTGTGAG 274

QY 22 IleAsnGluIle**Tyr 27

Db 275 ATTATGAGCTCGACCAAC 292

RESULT 30

LOCUS CF883054 682 bp mRNA linear EST 31-OCT-2003

DEFINITION trico32xk16.d11 T.reesei mycelial culture, Version 6 October 2003

ACCESSION Hypocrea jecorina cDNA clone trico32xk16, mRNA sequence.

VERSION CF883054

KEYWORDS EST

SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)

ORGANISM Hypocrea jecorina

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

1 (bases 1 to 682)

Hypocremetidae; Hypocreales; Hypocreaceae; Hypocrea.

Diener, S.E., Darkmeyer, L., Dunn-Coleman, N., Houfek, T.D.,

Mitchell, T.K., van Solingen, P., Teunissen, P.J.M., Ward, M. and

Dean, R.A.

Analysis of the protein processing and secretion pathways in a

Trichoderma reesei EST dataset

Unpublished (2003)

Contact: Ralph A. Dean

Fungal Genomics Laboratory

North Carolina State University

Campus Box 7251, Raleigh, NC 27695, USA

Tel: 919-513-0020

Fax: 919-513-0024

Email: ralph.dean@ncsu.edu

Seq primer: Tr-F1 primer.

Location/Qualifiers

1 682

/organism="Hypocrea jecorina"

/mol_type="mRNA"

/strain="Omega"

/db_xref="taxon:51453"

/clone="trico32xk16"

/dev_stage="mycelia"

/clone_lib="T.reesei mycelial culture, Version 6 October

2003"

/note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial

culture grown from 24 hrs to 6 days with varying Carbon

and Nitrogen sources and concentrations."

ORIGIN

Alignment Scores:

Pred. No.: 0.00746 Length: 682

Score: 80.00 Matches: 14

Percent Similarity: 78.57% Conservative: 8

Best Local Similarity: 50.00% Mismatches: 6

Query Match: 55.17% Indels: 0

DB: 14 Gaps: 0

US-09-987-190-2 (1-30) x CF883054 (1-682)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 20

Db 227 AAAGCAACCTCCCGAGCTGCGTACGACTAGCGGCGCTGAGCCTACATCTCGGAC 286

QY 21 GlnIleAsnGluIle**TyrThr 28

Db 287 AAGATCATGAGCTCCACCACTCA 310

RESULT 31

LOCUS CF873019 702 bp mRNA linear EST 31-OCT-2003

DEFINITION trico32xk16.b1 T.reesei mycelial culture, Version 6 October 2003

University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: JENREV (CAGGAACAGCTATGACC).

FEATURES

source
1..767
Location/Qualifiers
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="CCLONES"
/db_xref="taxon:3352"
/clone="RDR3_19_A06_A022"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="loblolly pine roots recovering from drought DR3"
/note="vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots recovering from drought. Water was withheld from ramet clones until predawn needle water potential reached -1.75 MPa. Plants were well watered on day 7 and allowed to recover for 2 days, at which time roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Alignment Scores:
Pred. No.: 0.00869 Length: 767
Score: 80.00 Matches: 15
Percent Similarity: 76.92% Conservative: 5
Best Local Similarity: 57.62% Mismatches: 6
Query Match: 55.17% Indels: 0
DB: 14 Gaps: 0

US-09-987-190-2 (1-30) x CF392896 (1-767)

Qy 2 TytSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyCln 21
Db 204 TTTAGTTTACGGAGCTTCATACGATACAGCGCATGGAAACCGTTATTAGTGGAG 263
Qy 22 IleAsnGluIle***Tyr 27
Db 264 ATTATGAGCTGCACAC 281

RESULT 34
CD467777
LOCUS
DEFINITION
LeukoS1_6_G06.g1_A023 Stimulated peripheral blood leukocytes S1
Equus caballus cDNA clone LeukoS1_6_G06_A023 5', mRNA sequence.
CD467777
ACCESSION
VERSION
CD467777.1 GI:31389045
KEYWORDS
EST.
SOURCE
Equus caballus (horse)
ORGANISM
Equus caballus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

REFERENCE
AUTHORS
Vandenplas, M., Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Moore, J.N., Liang, C., Sun, F., Sullivan, R., Shah, M. and Pratt, L.H.
An EST database from equine (Equus caballus) stimulated peripheral blood leukocytes
Unpublished (2003)
Other ESTs: LeukoS1_6_G06.b1_A023
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu

JOURNAL

COMMENT

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical

Science; tissue and RNA were prepared in the Department of Large Animal Medicine, University of Georgia; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: Sug5 (CTTCTGCTCTAAAAGCTGCG).

FEATURES
source
1..828
Location/Qualifiers
/organism="Equus caballus"
/mol_type="mRNA"
/strain="Belgian draft"
/db_xref="taxon:9796"
/clone="LeukoS1_6_G06_A023"
/sex="female"
/tissue_type="blood"
/cell_type="leukocytes"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Stimulated peripheral blood leukocytes S1"
/note="Organ: circulated system; Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The library was prepared from polyA+ RNA from equine peripheral blood leukocytes isolated from a healthy adult horse. The leukocytes were stimulated for 4 hr with 10 ng/ml E. coli 055:B5 LPS. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

ORIGIN

Alignment Scores:
Pred. No.: 0.0096 Length: 828
Score: 80.00 Matches: 13
Percent Similarity: 78.57% Conservative: 9
Best Local Similarity: 46.43% Mismatches: 6
Query Match: 55.17% Indels: 0
DB: 14 Gaps: 0

US-09-987-190-2 (1-30) x CD467777 (1-828)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 128 AAGCACAGCTCCCGAGCTTCAGTATGATATGCGCTCTGGAGCCCTACATCAAGCC 187
Qy 21 GlnIleAsnGluIle***TyrThr 28
Db 188 CAGATCATGAGCTGCACACAGC 211

RESULT 35
CA937400
LOCUS
DEFINITION
CA937400.y1 Gm-cl048 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl048-6005 5' similar to SW:SODM_PEA P27084 SUPEROXIDE DISMUTASE [MN], MITOCHONDRIAL PRECURSOR i, mRNA sequence.

ACCESSION
VERSION
CA937400.1 GI:27425880

KEYWORDS
EST.

SOURCE
Glycine max (soybean)

ORGANISM

Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE

AUTHORS

Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com

Seq primer: -40RP from Gibco
High quality sequence stop: 242.

FEATURES

source

```
1. .286
   /organism="Glycine max"
   /mol_type="mRNA"
   /db_xref="taxon:3847"
   /clone="SOYBEAN CLONE ID: Gm-cl048-6005"
   /tissue_type="whole seedlings of greenhouse grown plants"
   /dev_stage="1 week old"
   /lab_host="DH10B"
   /clone_lib="Gm-cl048"
   /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The Clark NIL was constructed and seed was provided
by Dr. J. Specht, University of Nebraska (Shoemaker and
Specht, 1995). The cDNA library was constructed from mRNA
isolated from whole seedlings of 1 week old greenhouse
grown plants. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site and a 3' anchor. EcoRI adapters were
ligated to the blunt-ended cDNA fragments followed by XhoI
digestion. The cDNA fragments were directionally cloned
into the EcoRI-XhoI restriction site of the pBluescript
vector. The ligated cDNA fragments were transformed into
DH10B host cells (GibcoBRL). The library was constructed
in cooperation with Dr. Paul Keim's laboratory at Northern
Arizona University."
```

ORIGIN

```
Alignment Scores:
Pred. No.: 0.00354 Length: 286
Score: 79.00 Matches: 13
Percent Similarity: 80.77% Conservative: 8
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 54.48% Indels: 0
DB: 14 Gaps: 0
```

US-09-987-190-2 (1-30) x CA937400 (1-286)

```
QY 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 117 TACACGCTCCCGATCTGGATTACGACTATGGCGCTCTGGAGCCAGCCATCAGCGGGAA 176
QY 22 IleAsnGluIle***Tyr 27
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 177 ATCATGCAGCTGCACCAC 194
```

RESULT 36

AW733168

LOCUS

DEFINITION

AW733168 306 bp mRNA linear EST 03-DEC-2001
Gm-cl016-9492 5', similar to SW:SODM_PEA P27084 SUPEROXIDE DISMUTASE
[MN] PRECURSOR ;, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE

1 (bases 1 to 306)

AUTHORS

Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.

TITLE

JOURNAL

COMMENT

Public Soybean EST Project
Published (1999)

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130

South Memorial Parkway Huntsville, AL 35801 For further information

call: (800)-533-4363 or contact via email: ccu@resgen.com

Insert Length: 1240 Std Error: 0.00

Seq primer: -40RP from Gibco

High quality sequence stop: 305.

FEATURES

source

```
1. .306
   /organism="Glycine max"
   /mol_type="mRNA"
   /db_xref="taxon:3847"
   /clone="GENOME SYSTEMS CLONE ID: Gm-cl016-9492"
   /tissue_type="immature flowers of field grown plants"
   /lab_host="Xl10-Gold"
   /clone_lib="Gm-cl016"
   /note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
XhoI; This cDNA library was constructed from mRNA isolated
from immature flowers of field grown plants. The cDNA
library was prepared using the Stratagene pBluescript II
XR library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(dT) sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed by
XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into Xl10-Gold host cells. This library was
constructed by Dr. Randy Shoemaker and Dr. John
Erpelting."
```

ORIGIN

```
Alignment Scores:
Pred. No.: 0.00386 Length: 306
Score: 79.00 Matches: 13
Percent Similarity: 80.77% Conservative: 8
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 54.48% Indels: 0
DB: 10 Gaps: 0
```

US-09-987-190-2 (1-30) x AW733168 (1-306)

```
QY 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 160 TACACGCTCCCGATCTGGATTACGACTATGGCGCTCTGGAGCCAGCCATCAGCGGGAA 219
QY 22 IleAsnGluIle***Tyr 27
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 220 ATCATGCAGCTGCACCAC 237
```

RESULT 37

CA910188

LOCUS

DEFINITION

CA910188 308 bp mRNA linear EST 27-DEC-2002
PCS01280X5F Scarlet Runner Bean Suspensor Region TripLex2 Phaseolus
coccineus cDNA 5', similar to Superoxide dismutase, mitochondrial
precursor, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

CA910188.1 GI:27397180
EST.

call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 2110 Std Error: 0.00
High quality sequence stop: 424.
Location/Qualifiers

FEATURES

source

1. .425
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl039-374"
/tissue_type="whole seedling without cotyledons"
/lab_host="DH10B"
/clone_lib="Gm-cl039"
/note="Vector: pBluescriptII SK+; Site 1: EcoRI; Site 2:
XhoI; This cDNA library was constructed from mRNA isolated
from 2 week old seedlings with the cotyledons removed at
the time of harvest. The seedlings for the cultivar Ogden
were grown in a growth chamber using germination paper.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with a XhoI restriction
site. EcoRI adapters were ligated to the blunt-ended cDNA
fragments followed by XhoI digestion. The cDNA fragments
were directionally cloned into the EcoRI-XhoI restriction
site of the pBluescript vector. The ligated cDNA fragments
were transformed into DH10B host cells (Gibco BRL). This
library was constructed by Dr. Randy Shoemaker."

ORIGIN

Alignment Scores:
Pred. No.: 0.00591 Length: 425
Score: 79.00 Matches: 13
Percent Similarity: 80.77% Conservative: 8
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 54.48% Indels: 0
DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x BE210200 (1-425)

QY 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
DB 159 TACACGCTCCCGATCTGTGATTACGACTATGGCGCTCTGGAGCCGCCATCAGCGGTGAA 219
QY 22 IleAsnGluIle***Tyr 27
DB 219 ATCATGAGCTGCACAC 236

Search completed: August 31, 2004, 21:57:15
Job time : 6697 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 24, 2004, 22:47:41 ; Search time 122 Seconds
(without alignments)
69.479 Million cell updates/sec

Title: US-09-987-190-2

Perfect score: 145

Sequence: 1 KYSLPELDYEFSGATEPIYISQINFIYTX 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003s:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	141	97.2	30	2	AAW53252
2	101	69.7	207	5	AA015875
3	100	69.0	233	5	AB05612
4	94	64.8	207	5	AA015874
5	79	54.5	30	2	AAW29762
6	79	54.5	224	2	AAW29771
7	77	53.1	200	4	AAU00514
8	77	53.1	200	4	AAU00514
9	74	51.0	95	5	AAE24641
10	74	51.0	101	3	AAU02172
11	74	51.0	155	4	AAU03130
12	74	51.0	183	2	AAE29656
13	74	51.0	198	1	AAE0603
14	74	51.0	198	1	AAE0602
15	74	51.0	198	2	AAE75191
16	74	51.0	198	2	AAE75192
17	74	51.0	198	3	AAE55846
18	74	51.0	199	2	AAE20015
19	74	51.0	199	2	AAE60359
20	74	51.0	222	1	AAE71701
21	74	51.0	222	2	AAE44801
22	74	51.0	222	2	AAE61337
23	74	51.0	222	2	AAE75193
24	74	51.0	222	2	AAE90713
25	74	51.0	222	2	AAW00018

26	74	51.0	222	2	AAW00453	Human man
27	74	51.0	222	2	AAW96317	Human man
28	74	51.0	222	2	AAW82446	Human mso
29	74	51.0	222	2	AAW98177	Human man
30	74	51.0	222	2	AAW98175	Human man
31	74	51.0	222	2	AAW98172	Human man
32	74	51.0	222	2	AAW98171	Human man
33	74	51.0	222	2	AAW98170	Human nat
34	74	51.0	222	2	AAW98174	Human man
35	74	51.0	222	2	AAW98169	Human nat
36	74	51.0	222	2	AAW98173	Human nat
37	74	51.0	222	2	AAW98176	Human man
38	74	51.0	222	3	AAW08206	Human man
39	74	51.0	222	3	AAW08205	A modifie
40	74	51.0	222	3	AAW08204	Q143N mod
41	74	51.0	222	5	ABW79798	Amino aci
42	74	51.0	222	5	ABW79798	Human man
43	74	51.0	222	7	ADD45869	Human man
44	74	51.0	223	1	AAW90551	Rat Prote
45	74	51.0	226	3	AAW55849	Human man

ALIGNMENTS

RESULT 1
AAW53252
ID AAW53252 standard; protein; 30 AA.

XX AC AAW53252;

DT 30-JUL-1998 (first entry)

XX Candida albicans allergen - antigenic protein SEQ ID NO:2.

KW Candida albicans; vaccine; allergen; antigenic protein; fungal antigen; immune response; infection; insoluble.

OS Candida albicans.

XX Key Location/Qualifiers

FT Misc-difference 26 /note= "any amino acid"

FT Misc-difference 23 /note= "any amino acid"

FT Misc-difference 30 /note= "any amino acid"

XX WO9809990-A1.

XX 12-MAR-1998.

XX 29-AUG-1997; 97WO-JP003041.

XX 04-SEP-1996; 96JP-00255400.

XX 31-MAR-1997; 97JP-00099775.

XX (TAKI) TAKARA SHUZO CO LTD.

XX Takesako K, Mizutani S, Endo M, Kato I;

XX WPI; 1998-193553/17.

XX Fungal antigens comprising insoluble fraction of fungal cells - useful for, e.g. stimulating immune response and treatment and diagnosis of fungal infection(s).

XX Claim 26; Page 75; 108pp; Japanese.

XX The present sequence represents an active vaccine component or allergen derived from Candida albicans, which is an antigenic protein. The present invention describes fungal antigens, comprising the insoluble fraction of fungal cells having completely/partially removed cell walls. Also

DT 16-JAN-2003 (first entry)
 XX Mycobacterium tuberculosis soda protein.
 DE
 XX
 XX Mycobacterium detection method; soda; sod; pncA.
 KW
 XX Mycobacterium tuberculosis.
 OS
 XX WO200274991-A2.
 PN
 XX 26-SEP-2002.
 PD
 XX 20-MAR-2002; 2002WO-GB001308.
 PF
 XX 20-MAR-2001; 2001GB-00006949.
 PR
 XX (NORC-) NORCHIP AS.
 PA (ALLA/) ALLARD S J.
 PA
 XX Karlsen F;
 PI
 XX WPI; 2002-750564/B1.
 DR N-PSDB; ABT12954.
 XX
 XX Detecting the presence of Mycobacterium tuberculosis in a test sample,
 PT comprises inducing mRNA expression of Mycobacterium tuberculosis and
 PT detecting the induced mRNA.
 XX
 PS Example 5; Page 56-57; 70pp; English.
 XX
 CC The invention comprises a method for detecting the presence of a micro-
 CC organism (particularly Mycobacterium tuberculosis) in a test sample. The
 CC method of the invention comprises exposing the test sample to an inducer
 CC that is capable of inducing the expression of at least one gene in the
 CC micro-organism and then testing for the presence of mRNA from this gene.
 CC The method of the invention is useful for detecting an mRNA that is
 CC expressed in a species of Mycobacterium (e.g. Mycobacterium
 CC tuberculosis). The present amino acid sequence represents a Mycobacterium
 CC protein which was used in an example of the invention
 XX
 XX Sequence 207 AA;
 SQ
 Query Match 64.8%; Score 94; DB 5; Length 207;
 Best Local Similarity 53.6%; Pred. No. 5.1e-07;
 Matches 15; Conservative 10; Mismatches 3; Indels 0; Gaps 0;
 QY 1 KYSLPELDYFSGATEPYISQINEIXYT 28
 Db :||:||||:| ||:|||||: :
 3 EYTLPLDWDYGALEPHISQINELHHS 30
 RESULT 5
 AAW29762
 ID AAW29762 standard; peptide; 30 AA.
 XX
 AC AAW29762;
 XX
 DT 27-AUG-2003 (revised)
 DT 20-FEB-1998 (first entry)
 DE Malassezia fungus MF-4 antigenic peptide.
 XX
 KW Malassezia; fungus; antigenic; human; IgE, immunoglobulin E; antibody;
 KW allergy; antigen.
 XX
 OS Malassezia.
 PN WO9721817-A1.
 XX
 PD 19-JUN-1997.
 PF 10-DEC-1996; 96WO-JP003602.
 XX
 XX 12-DEC-1995; 95JP-00346627.
 PR 05-SEP-1996; 96JP-00257612.
 PR 05-SEP-1996; 96JP-00257613.
 XX
 XX (TAKI) TAKARA SHUZO CO LTD.
 PA Takesako K, Okado T, Yagihara T, Kuroda M, Onishi Y, Kato I;
 PI Akiyama K, Yasueda H, Yamaguchi H;
 XX WPI; 1997-332788/30.
 DR N-PSDB; AAT85877.
 XX
 XX Antigenic proteins from the fungus Malassezia - bind to IgE antibodies
 PT present in patients with Malassezia allergies, useful for diagnosis,
 PT treatment and prevention of such conditions.

PR 12-DEC-1995; 95JP-00346627.
 PR 05-SEP-1996; 96JP-00257612.
 PR 05-SEP-1996; 96JP-00257613.
 XX
 XX (TAKI) TAKARA SHUZO CO LTD.
 PA Takesako K, Okado T, Yagihara T, Kuroda M, Onishi Y, Kato I;
 PI Akiyama K, Yasueda H, Yamaguchi H;
 XX WPI; 1997-332788/30.
 DR
 XX Antigenic proteins from the fungus Malassezia - bind to IgE antibodies
 PT present in patients with Malassezia allergies, useful for diagnosis,
 PT treatment and prevention of such conditions.
 XX
 PS Claim 8; Page 113; 162pp; Japanese.
 XX
 CC The present sequence represents a specifically claimed antigenic peptide
 CC isolated from the fungus Malassezia. The antigenic peptide can bind to
 CC IgE antibodies present in patients with allergic conditions. Antigenic
 CC proteins, peptides and nucleic acids from the fungus Malassezia can be
 CC used in the diagnosis, treatment and prevention of allergic conditions
 CC due to Malassezia organisms (such as M.furur, M. sympodialis and
 CC M.pachydermatitis). (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 30 AA;
 Query Match 54.5%; Score 79; DB 2; Length 30;
 Best Local Similarity 55.6%; Pred. No. 1.4e-05;
 Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 1 KYSLPELDYFSGATEPYISQINEIXY 27
 Db ||:||||:| ||:|||||: |
 1 KYTLPLPYDYGALPAISGEIMETHY 27
 RESULT 6
 AAW29771
 ID AAW29771 standard; protein; 224 AA.
 XX
 AC AAW29771;
 XX
 DT 27-AUG-2003 (revised)
 DT 23-FEB-1998 (first entry)
 XX
 DE Malassezia fungus MF-4 antigenic protein.
 XX
 KW Malassezia; fungus; antigenic; human; IgE, immunoglobulin E; antibody;
 KW allergy; antigen.
 XX
 OS Malassezia.
 PN WO9721817-A1.
 XX
 PD 19-JUN-1997.
 PF 10-DEC-1996; 96WO-JP003602.
 XX
 XX 12-DEC-1995; 95JP-00346627.
 PR 05-SEP-1996; 96JP-00257612.
 PR 05-SEP-1996; 96JP-00257613.
 XX
 XX (TAKI) TAKARA SHUZO CO LTD.
 PA Takesako K, Okado T, Yagihara T, Kuroda M, Onishi Y, Kato I;
 PI Akiyama K, Yasueda H, Yamaguchi H;
 XX WPI; 1997-332788/30.
 DR N-PSDB; AAT85877.
 XX
 XX Antigenic proteins from the fungus Malassezia - bind to IgE antibodies
 PT present in patients with Malassezia allergies, useful for diagnosis,
 PT treatment and prevention of such conditions.

XX Claim 38; Page 85-86; 162pp; Japanese.

XX The present sequence represents a specifically claimed antigenic protein

CC isolated from the fungus *Malassezia*. The antigenic protein can bind to

CC IgE antibodies present in patients with allergic conditions. Antigenic

CC proteins, peptides and nucleic acids from the fungus *Malassezia* can be

CC used in the diagnosis, treatment and prevention of allergic conditions

CC due to *Malassezia* organisms (such as M.furfur, M. sympodialis and

CC M.pachydermatitis). (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 224 AA;

Query Match 54.5%; Score 79; DB 2; Length 224;

Best Local Similarity 55.6%; Pred. No. 0.00017;

Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 KYSLPELDYFSAATEPYISQINEIXY 27

DB 25 KYTLPLPDYDGALEPAISGEIMETHY 51

RESULT 7

AAU00514

ID AAU00514 standard; protein; 200 AA.

XX AC

XX AAU00514;

DT 09-MAY-2001 (first entry)

XX DE

XX C. melassecola superoxide dismutase.

XX Superoxide dismutase; sod; coryneform microorganism; metabolite; vitamin;

XX D-pantothenic acid; L-lysine; amplification; animal nutrition.

XX OS

XX Corynebacterium melassecola.

XX EP1077261-A2.

XX 21-FEB-2001.

XX 02-AUG-2000; 2000EP-00116669.

XX 13-AUG-1999; 99US-00373731.

XX (DEGS) DEGUSSA-HUELS AG.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Merkamm M, Guyonvarch A, Marx A;

XX WPI; 2001-212718/22.

XX N-PSDB; AAS00520.

XX New DNA encoding superoxide dismutase of Corynebacterium, useful for

XX producing transformants with increased production of metabolites,

XX particularly lysine.

XX Claim 3; Page 14-15; 19pp; English.

XX The sequence represents Corynebacterium melassecola superoxide dismutase

XX (sod) polypeptide. Coryneform microorganisms may be transformed with a

XX sod DNA sequence and the sod gene can be amplified. Sod is then often

XX overexpressed in coryneform bacteria. Coryneforms that overexpress sod

XX are used for production of metabolites, particularly nucleotides,

XX vitamins and amino acids, especially D-pantothenic acid or, specifically,

XX L-lysine. These metabolites are useful in human or animal nutrition and

XX as pharmaceuticals. Overexpression of sod in coryneforms increases the

XX yield of particular metabolites

XX Sequence 200 AA;

Query Match 53.1%; Score 77; DB 4; Length 200;

Best Local Similarity 48.1%; Pred. No. 0.00032;

Matches 13; Conservative 7; Mismatches 0; Gaps 0;

QY 2 YSLPELDYFSAATEPYISQINEIXY 28

DB 4 YELPELDYDAYDALEPHIAAEIMELHHS 30

RESULT 8

AAG92973

ID AAG92973 standard; protein; 200 AA.

XX AC

XX AAG92973;

DT 26-SEP-2001 (first entry)

XX DE

XX C glutamicum protein fragment SEQ ID NO: 6727.

XX Coryneform bacterium; amino acid synthesis; vitamin; saccharide;

XX organic acid synthesis.

XX OS

XX Corynebacterium glutamicum.

XX EP1108790-A2.

XX 20-JUN-2001.

XX 18-DEC-2000; 2000EP-00127688.

XX 16-DEC-1999; 99JP-00377484.

XX 07-APR-2000; 2000JP-00159162.

XX 03-AUG-2000; 2000JP-00280988.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;

XX Tateishi N, Senoh A, Ikeda M, Ozaki A;

XX WPI; 2001-376931/40.

XX N-PSDB; AAH68192.

XX Novel polynucleotides derived from Coryneform bacteria, for identifying

XX mutation point of a gene, measuring expression of a gene, analyzing

XX expression profile or pattern of a gene and identifying homologous gene.

XX Claim 17; SEQ ID NO 6727; 246pp + Sequence Listing; English.

XX The present invention provides a number of nucleotide and protein

XX sequences from the Coryneform bacterium Corynebacterium glutamicum. These

XX are useful for identifying the mutation point of a gene derived from a

XX mutant of coryneform bacterium, measuring expression amount and analysing

XX the expression profile or expression pattern of a gene derived from

XX Coryneform bacterium, and identifying a homologue of a gene derived from

XX coryneform bacterium. Coryneform bacteria are useful for producing amino

XX acids, nucleic acids, vitamins, saccharides and organic acids,

XX particularly L-lysine. The present sequence is a protein described in the

XX exemplification of the invention. Note: The sequence data for this patent

XX did not form part of the printed specification, but was obtained in

XX electronic format directly from the European Patent Office

XX Sequence 200 AA;

Query Match 53.1%; Score 77; DB 4; Length 200;

Best Local Similarity 48.1%; Pred. No. 0.00032;

Matches 13; Conservative 7; Mismatches 0; Gaps 0;

QY 2 YSLPELDYFSAATEPYISQINEIXY 28

DB 4 YELPELDYDAYDALEPHIAAEIMELHHS 30

RESULT 9

AAE24641

ID AAE24641 standard; protein; 95 AA.

PR 26-JAN-2001; 2001US-00770160.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Drmanac RT;
 XX WPI; 2001-611725/70.
 DR Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy.
 XX
 PS Claim 20; Page 248; 765pp; English.
 XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising the
 CC nucleic acids encoding the polypeptides and cells genetically engineered
 CC to express them are also useful for producing the proteins. The proteins
 CC are useful in genetic vaccination, testing and therapy, and can be used
 CC as nutritional supplements. They may be used to increase stem cell
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 CC and/or nerve tissue growth or regeneration; immune suppression and/or
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
 CC AAU29510-AAU33304 represent the amino acid sequences of novel human
 CC secreted proteins of the invention
 XX
 SQ Sequence 155 AA;
 Query Match 51.0%; Score 74; DB 4; Length 155;
 Best Local Similarity 42.9%; Pred. No. 0.00072;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
 QY 1 KYSLPELDYFESATEPYISGQINEIXYT 28
 Db 50 KHSPLDLPYDYGALPHINAQIMQLHHS 77
 RESULT 12
 AAY29656
 ID AAY29656 standard; protein; 183 AA.
 AC AAY29656;
 XX 03-NOV-1999 (first entry)
 DT Human manganese superoxide dismutase exon 3-deleted isoform protein.
 XX
 DE Human, manganese superoxide dismutase; MnSOD; exon 3 deleted isoform;
 XX MnSOD E3(-); diagnosis; viral infection; HIV; oncogenesis; tumour;
 KW UV-induced damage; post ischaemia reperfusion damage; anti-inflammatory;
 KW cytotoxic; cardiotoxic; cancer.
 XX
 XX Homo sapiens.
 OS Synthetic.
 XX W09943697-A1.
 PN 02-SEP-1999.
 XX
 FD 25-FEB-1999; 99WO-US004129.
 XX
 PF 25-FEB-1998; 98US-0075948P.
 XX
 PR (UYCO-) UNIV & COMMUNITY COLLEGE.
 PA Anziano PQ;
 XX WPI; 1999-527592/44.
 DR

DR N-PSDB; AAZ08755.
 XX A new isoform useful for diagnosing oxidative stress, and treating viral
 PT infections.
 XX
 PS Claim 1; Page 12; 64pp; English.
 XX
 CC The present sequence represents an isoform of manganese superoxide
 CC dismutase (MnSOD), which is a splice-variant lacking exon 3 of the full
 CC length MnSOD (i.e. MnSOD E3(-)). MnSOD E3(-) may be useful in the
 CC treatment of a wide variety of disorders including viral infections,
 CC particularly HIV, and may be used for the prevention of oncogenesis,
 CC tumour promotion and invasiveness, and UV-induced damage, for protection
 CC of cardiac tissue against post ischaemia reperfusion damage, as an anti-
 CC inflammatory agent, to reduce the cytotoxic and cardiotoxic effects of
 CC anti-cancer drugs, and to improve the longevity of living cells
 XX
 SQ Sequence 183 AA;
 Query Match 51.0%; Score 74; DB 2; Length 183;
 Best Local Similarity 42.9%; Pred. No. 0.00088;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
 QY 1 KYSLPELDYFESATEPYISGQINEIXYT 28
 Db 25 KHSPLDLPYDYGALPHINAQIMQLHHS 52
 RESULT 13
 AAP80603
 ID AAP80603 standard; protein; 198 AA.
 XX AAP80603;
 XX 25-MAR-2003 (revised)
 DT 03-OCT-1990 (first entry)
 XX
 DE Sequence of polypeptide of Formula IVb encoding modified portion of human
 DE manganese superoxide dismutase (hMnSOD).
 XX
 KW Human manganese superoxide dismutase derivative; clone BS8; formula IVb;
 KW enzyme; EC-1.15.1.1.
 XX
 OS Homo sapiens.
 XX EP282899-A.
 PN 21-SEP-1988.
 PD 10-MAR-1988; 88EP-00103754.
 PF 14-MAR-1987; 87DE-03708306.
 PR 26-MAY-1987; 87DE-03717695.
 PR 10-JUL-1987; 87DE-03722884.
 PR 24-DEC-1987; 87DE-03744038.
 XX
 XX (BOEH) BOEHRINGER INGELHEIM.
 PA Heckl K, Spevak W, Ostermann E, Zophel A, Krystek E;
 XX Maurerfoggy I, Wichcasta MJ, Stralow C;
 PI WPI; 1988-265361/38.
 DR N-PSDB; AAN81219.
 XX
 XX Prodn. of human manganese superoxidisedismutase peptide(s) - and DNA coding
 PT sequences, for control and diagnosis of e.g. inflammatory diseases.
 XX
 PS Disclosure; Page 10; 57pp; German.
 XX The patent is for polypeptides, esp. non-glycosylated, having the
 CC enzymatic, biological and immunological properties of hMnSOD that are
 CC prepd. by genetic engineering methods. Also new are DNA sequences
 CC encoding all or part of the polypeptides and replicating vectors,

XX	Sequence 198 AA;
SQ	
	Query Match 51.0%; Score 74; DB 2; Length 198; Best Local Similarity 42.9%; Pred. No. 0.00098; Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
QY	1 KYSLELDVFSATPYPISGQINEIXYT 28 :: : :: :~::~:
Dd	1 KHSLPDLPDYGALEPHINAQMQLHHS 28 :: : :: :~::~:
RESULT 16	
AAR75192	
ID	AAR75192 standard; protein; 198 AA.
XX	
AC	AAR75192;
XX	
DT	25-MAR-2003 (revised)
DT	17-MAY-1996 (first entry)
XX	
DE	Human manganese superoxide dismutase (Gln29).
XX	
KW	hMn-SOD; manganese; superoxide dismutase; MnSOD; ECSOD; proteoglycan; human; autoimmune disease; rheumatoid arthritis; neoplasm; emphysema;
KW	osteoarthritis; wound healing.
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
Modified-site	39..41 /label= N-glycosylation_site /note= "potential"
Modified-site	73..75 /label= N-glycosylation_site /note= "potential"
Modified-site	80..82 /label= N-glycosylation_site /note= "potential"
Modified-site	188..190 /label= N-glycosylation_site /note= "potential"
EP676472-A1.	
11-OCT-1995.	
10-MAR-1988;	95EP-00107460.
14-MAR-1987;	87DB-03708306.
26-MAY-1987;	87DE-03717695.
10-JUL-1987;	87DE-03722884.
24-DEC-1987;	87DE-03744038.
(BOEH) BOEHRINGER INGELHEIM INT GMBH.	
Heckl K, Spevak W, Ostermann E, Zoephel A, Krystek E; Maurer-Fogy I, Wiche-Castanon M, Stratowa C, Hauptmann R;	
WPI: 1995-346092/45. N-PSDB; RAQ94272.	
Genes encoding recombinant human manganese superoxide dismutase - for treatment, prevention and diagnosis of inflammatory diseases.	
Claim 1; Page 9-10; 54pp; German.	
The present sequence is that of the 198 amino acid long hMn-SOD mature polypeptide having a Gln residue at position 29. The protein is produced with an N-terminal Met residue which is then removed, e.g by treatment with CNBr or CNCl, to release mature hMn-SOD. The mature recombinant protein is useful for treating, preventing or diagnosing inflammatory, degenerative, neoplastic and rheumatic disorders; in wound healing and autoimmune diseases. (Updated on 25-MAR-2003 to correct PF field.)	

XX	Sequence 198 AA;
SQ	
	Query Match 51.0%; Score 74; DB 2; Length 198; Best Local Similarity 42.9%; Pred. No. 0.00098; Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
QY	1 KYSLELDVFSATPYPISGQINEIXYT 28 :: : :: : : : : : : :~::~:
Dd	1 KHSLPDLPDYGALEPHINAQMQLHHS 28 :: :~::~:
RESULT 17	
AAY55846	
ID	AAY55846 standard; protein; 198 AA.
XX	
AC	AAY55846;
XX	
DT	06-MAR-2000 (first entry)
XX	
DE	Human manganese superoxide dismutase (MnSOD) protein.
XX	
KW	Manganese superoxide dismutase; MnSOD; ECSOD; proteoglycan; human; endotheial; oxidative damage; pulmonary inflammatory injury; cancer; lung disease; hypoxia; ischemia; reperfusion injury; arthritis; hyperoxia; atherosclerosis; lupus erythematosus; hypertension; neutrophil-mediated inflammation.
OS	Homo sapiens.
XX	
PN	WO958547-A1.
XX	
PD	18-NOV-1999.
XX	
PF	06-MAY-1999; 99WO-US009921.
XX	
PR	08-MAY-1998; 98US-00075019.
XX	(WEBB-) WEBB-WARING INST BIOMEDICAL RES.
XX	Mccord JM, Gao B, Flores SC;
XX	WPI: 2000-062283/05. N-PSDB; AAZ39779.
DR	
XX	Modified manganese superoxide dismutase, methods of production and antibodies.
PT	
XX	
PS	Claim 29; Page 71-72; 83pp; English.
CC	The invention provides a nucleic acid molecule encoding a genetically modified manganese superoxide dismutase (MnSOD). The nucleic acid comprises: a first nucleic acid sequence encoding an enzymatically active portion of MnSOD; and a second nucleic acid sequence encoding a peptide (ECSOD) that binds to polyanionic polysaccharides or proteoglycans on endothelial cell surfaces. The protein protects a mammal, especially humans, from oxidative damage and especially from conditions consisting of pulmonary inflammatory injury, lung disease, cancer, hypoxia, ischemia of reperfusion injury, hyperoxia, atherosclerosis, arthritis, lupus erythematosus, hypertension and neutrophil-mediated inflammation. The lung disease is infant or adult respiratory distress syndrome, interstitial lung disease or asthma. The mutant MnSOD also protects organs of mammals from pre- and post-transplantation oxidative damage. MnSOD is positively charged at physiological pH and has a longer plasma half-life of about 4 hours compared to 6-15 minutes for cytosolic Cu,Zn SOD (following intravenous injection). ECSOD has a substantial advantage over both Cu,ZnSOD and MnSOD because of its ability to bind to the endothelium. ECSOD is hard to produce in mammalian cell culture systems, so a fusion of ECSOD and MnSOD therefore overcomes these problems. The present sequence represents the human MnSOD protein
XX	Sequence 198 AA;
SQ	

XX Expression plasmid in Escherichia coli host system - encodes human
PT manganese superoxidodismutase analogue, useful for e.g. treating
PT inflammation.
XX
PS Claim 1; Fig 1a-1c; 27pp; English.
XX
CC The sequence is of a maganese superoxide dismutase which can be used to
CC catalyse the reduction of superoxide (SO) radicals to hydrogen peroxide
CC and molecular oxygen. It can be used to reduce reperfusion injury
CC following ischaemia and prolong the survival of excised organs. It can
CC also me used as a long acting anti-inflammatory drug. (Updated on 25-MAR-
CC 2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 222 AA;

Query Match 51.0%; Score 74; DB 2; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0011;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSSATEPYISQINEIXYT 28
Db 25 KHSLPDLPYDYGALPHINAQIMQLHHS 52

RESULT 22
AAR61337
ID AAR61337 standard; protein; 222 AA.
XX
AC AAR61337;
XX
DT 25-MAR-2003 (revised)
DT 31-MAY-1995 (first entry)
XX
DE Human manganese-contg. superoxide dismutase SOD-2.
XX
KW Human superoxide dismutase; hSOD2; mSOD; neurodegeneration;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW Hallervorden-Spatz disease; olivopontocerebellar atrophy;
KW familial amyotrophic lateral sclerosis; FALS; diagnosis; mutant SOD;
KW reverse transcription polymerase chain reaction; SSCP analysis.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Peptide 1..18
FT /label= signal peptide
FT Protein 19..222
FT /label= mature_mSOD
XX
XX WO9419493-A1.
XX
XX 01-SEP-1994.
XX
XX 28-FEB-1994; 94WO-US002089.
XX
XX 26-FEB-1993; 93US-00023980.
XX
XX (GEO) GEN HOSPITAL CORP.
XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX
XX Brown R, Horvitz HR, Rosen DR;
XX
XX WPI; 1994-294353/36.
XX N-PSDB; AAQ67474.
XX
XX Diagnosis, treatment and prevention of diseases of cell death - e.g.
XX amyotrophic lateral sclerosis, which are the result of e.g. decreased SOD
XX activity.
XX
XX Claim 22; Fig 3; 94pp; English.
XX
XX The presence of a mutation in a gene encoding a superoxide dismutase
CC

PF 20-NOV-1986; 86BE-00905796.
XX
XX
PR 22-NOV-1985; 85US-00801051.
PR 22-NOV-1985; 85US-00801090.
PR 12-SEP-1986; 86US-00907051.
XX
XX (BIOT-) BIO-TECHNOL GEN.
XX
XX WPI; 1987-101441/15.
XX N-PSDB; AAN71370.
XX
XX New DNA coding for polypeptide of human manganese superoxidodismutase -
PT useful e.g. for treating inflammation, and new expression vectors and
PT transformed cells.
XX
XX
PS Disclosure; Fig 1; 46pp; French.
XX
XX This sequence comprises both prepro- and mature-manganese super- oxide
CC dismutase (MSOD). It is encoded by the sense strand of a double-stranded
CC molecule contained in a recombinant vehicle. This recombinant MSOD
CC catalyses the reaction of hydrogen ions and the SOD radical anion to form
CC hydrogen peroxide and water. It is useful in veterinary and
CC pharmaceutical compsns. for eg reducing lesions of reperfusion following
CC ischaemia, to prolong survival time isolated organs and for treating
CC inflammation. See also AAN71371-72. (Updated on 10-MAR-2003 to add
CC missing OS field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 222 AA;

Query Match 51.0%; Score 74; DB 1; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0011;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSSATEPYISQINEIXYT 28
Db 25 KHSLPDLPYDYGALPHINAQIMQLHHS 52

RESULT 21
AAR44801
ID AAR44801 standard; protein; 222 AA.
XX
AC AAR44801;
XX
XX
DT 25-MAR-2003 (revised)
DT 21-JUN-1994 (first entry)
XX
DE MnSOD cDNA.
XX
KW MnSOD; manganese superoxide dismutase; N-terminal; catalyst; reperfusion;
KW injury; ischaemia; superoxide; SO; molecular oxygen; anti-inflammatory;
KW ss.
XX
XX Homo sapiens.
XX
XX US5270195-A.
XX
XX 14-DEC-1993.
XX
XX 10-JUL-1992; 92US-00912213.
XX
XX 22-NOV-1985; 85US-00801090.
XX 12-SEP-1986; 86US-00907051.
XX 29-OCT-1986; 86IE-00002851.
XX 27-MAR-1987; 87US-00032734.
XX 13-DEC-1989; 89US-00453057.
XX
XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
XX
XX Beck Y, Hartman JR;
XX
XX WPI; 1993-404931/50.
XX N-PSDB; AAQ53193.
XX
XX

CC (SOD1, SOD2 or SOD3) indicates an increased likelihood of developing a
 CC cell death disease, specifically a neurodegenerative disease. The use of
 CC SOD polypeptides to treat amyotrophic lateral sclerosis and diseases
 CC involving a deleterious mutation in the glutathione peroxidase-encoding
 CC gene, the catalase-encoding gene and the nitric oxide-encoding gene is
 CC claimed. The specification includes the sequences of human SOD1, hSOD2
 CC and hSOD3 (AAR61336- AAR61338, respectively). (Updated on 25-MAR-2003 to
 CC correct PN field.)

XX SQ Sequence 222 AA;

Query Match 51.0%; Score 74; DB 2; Length 222;
 Best Local Similarity 42.9%; Pred. No. 0.0011;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSSATEPYISQINEIXYT 28
 Db 25 KHSLPDLFDYDGALEPHINAQIMQLHHS 52

RESULT 23

AAR75193
 ID AAR75193 standard; protein; 222 AA.

AC AAR75193;

XX 25-MAR-2003 (revised)

DT 23-MAY-1996 (first entry)

XX Human manganese superoxide dismutase (lys29) preprotein.

KW hMn-SOD; manganese; superoxide dismutase; tetramer; inflammation;
 KW autoimmune disease; rheumatoid arthritis; neoplasm; emphysema;
 KW osteoarthritis; wound healing; leader peptide; precursor.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..24
 FT Protein /label= leader

FT /label= mature_hMnSOD_(Lys29)

PN EP676472-A1.

XX 11-OCT-1995.

PF 10-MAR-1988; 95EP-00107460.

PR 14-MAR-1987; 87DE-03708306.

PR 26-MAY-1987; 87DE-03717695.

PR 10-JUL-1987; 87DE-03722884.

PR 24-DEC-1987; 87DE-03744036.

XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.

PI Heckl K, Spevak W, Ostermann E, Zoepfel A, Kryetsek E;
 PI Maurer-Fogy I, Wiche-Castanon M, Strätowa C, Hauptmann R;

DR WPI; 1995-346092/45.

DR N-PSDB; AAQ94284.

PT Genes encoding recombinant human manganese superoxide dismutase - for
 PT treatment, prevention and diagnosis of inflammatory diseases.

PS Claim 8; Page 3-4 and Page 19-20; 54pp; German.

XX The present sequence is that of the 198 amino acid long hMn-SOD mature
 CC polypeptide having a Lys residue at position 29, preceded by a 24 amino
 CC acid residue leader peptide. Mature, recombinant hMn-SOD is useful for
 CC treating, preventing or diagnosing inflammatory, degenerative, neoplastic
 CC and rheumatic disorders; in wound healing and in autoimmune diseases.
 CC (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 222 AA;

Query Match 51.0%; Score 74; DB 2; Length 222;
 Best Local Similarity 42.9%; Pred. No. 0.0011;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSSATEPYISQINEIXYT 28
 Db 25 KHSLPDLFDYDGALEPHINAQIMQLHHS 52

RESULT 24

AAR90713

ID AAR90713 standard; protein; 222 AA.

XX AAR90713;

DT 25-MAR-2003 (revised)

DT 06-APR-1996 (first entry)

XX Human manganese superoxide-dismutase.

KW Human; manganese superoxide-dismutase; T-lymphocyte; probe; cDNA;
 KW Escherichia coli; plasmid pMS8-4; N-terminal truncation; cloning;
 KW aminopeptidase; antiinflammatory; oxygen free radical scavenger;
 KW synovial inflammation; arthritis; lung fibrosis.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..24

FT Region /note= "Pre-peptide"

FT /note= "39..48"

FT Misc-difference 66 /note= "Region used to construct probe AAT15591"

FT Misc-difference 112 /note= "Gln in previously published sequence"

FT Misc-difference 132 /note= "Gln in previously published sequence"

FT Misc-difference 147..148 /note= "Gln in previously published sequence"

FT /note= "Residues not present in previously published
 FT sequence"
 FT 203..213

FT Region /note= "Region used to construct probe AAT15592"

XX EP691401-A1.

XX 10-JAN-1996.

XX 25-MAR-1988; 95EP-00106995.

PR 27-MAR-1987; 87US-00032734.

PR 26-FEB-1988; 88US-00161117.

XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.

PI Hartman JR, Beck Y, Nimrod A;

DR WPI; 1996-059735/07.

DR N-PSDB; AAT15589.

PT New human manganese superoxide dismutase analogues - having a Lys and
 PT opt. His residue absent from the N-terminus, useful for treating e.g.
 PT synovial inflammation, arthritis or lung fibrosis.

XX Example 1; Fig 1; 45pp; English.

XX The sequence represents a human manganese superoxide-dismutase (MnSOD),
 CC and is encoded by a human T-lymphocyte cDNA isolated from a library in
 CC phage lambda-gt10 in Escherichia coli, by screening with a 5'-probe
 CC (AAT15591) and a 3'-probe (AAT15592), followed by subcloning in plasmid

AAW96317
ID AAW96317 standard; protein; 222 AA.
XX AC AAW96317;
XX DT 28-JUN-1999 (first entry)
XX DE Human manganese containing superoxide dismutase (MnSOD).
XX KW Manganese containing superoxide dismutase; MnSOD; IDDM;
KW diabetes mellitus; treatment; therapy; nitric oxide; NO; beta cell;
KW fatty acid; lipotoxic; cytotoxic; cytokine; osteoporosis;
KW inflammatory disease; autoimmune disease; neurodegenerative disease.
XX OS Homo sapiens.
PX PN W09906059-A2.
XX PD 11-FEB-1999.
XX PF 30-JUL-1998; 98WO-US015781.
XX PR 30-JUL-1997; 9TUS-0055092P.
PR 03-MAR-1998; 98US-0076676P.
XX (TEXA) UNIV TEXAS SYSTEM.
FA (BETA-) BETAGENE INC.
PI Hohmeier H, Thigpen A, Clark SA, Newgard CB, Unger RH;
PI Shimabukuro M, Koyama K, Ohneda M, Lee Y;
DR WPI; 1999-153448/13.
DR N-ESDB; AAX08429.
PT Protection of mammalian cells against immunotoxicity or lipotoxicity -
PT used for treating e.g. diabetes, obesity, wasting syndromes,
PT osteoporosis, inflammatory diseases, autoimmune diseases or
PT neurodegenerative diseases.
XX Disclosure; Page 233-234; 253pp; English.
PX PS Manganese containing superoxide dismutase (MnSOD) can be used to protect
CC cells against cytokine mediated killing. Inhibition of cytokine mediated
CC immunotoxicity of cells can be achieved by blocking free radical
CC production or the accumulation of free radicals in that cell. Treatment
CC of insulin dependent diabetes mellitus (IDDM) can be achieved by
CC blocking nitric oxide (NO) production in a pancreatic beta cell and by
CC providing a composition comprising an agent that reduces levels of fatty
CC acids in the cells and protects beta-cells of the subject against lipid-
CC mediated cell death. Cells can also be protected against nitric oxide
CC mediated cytotoxicity by introducing into the cell an antioxidant
CC agent. The methods can be used for protecting cells against
CC immunotoxicity mediated by, e. g. 1L-1 beta, 1L-1 alpha, gamma IFN, TNF
CC alpha, TNF beta, IL-8, IL-2, IL-6, IL-2, IL-3, IL-5, IL-7, IL-9, IL-14,
CC IL-17, granulocyte-macrophage colony stimulating factor or monocyte
CC chemoattractant protein-1. The methods can be used for the treatment of
CC e.g. insulin-dependent diabetes mellitus (IDDM), NIDDM, obesity, wasting
CC syndromes, short stature, osteoporosis, inflammatory diseases, autoimmune
CC diseases, or neurodegenerative diseases
XX SQ Sequence 222 AA;
Query Match 51.0%; Score 74; DB 2; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0011;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0
QY 1 KYSLPELDYFSATEPYISGQINEIXYT 28
Db : : : :
25 KHSLPDLPDYDYGALPHINAQMQLHHS 52
RESULT 28
AAN92446

FT	Active-site	50	/note= "mature protein"
FT	FT		
FT	FT		
FT	Misc-difference	54	/note= "His-26"
FT	FT		
FT	FT		
FT	Active-site	54	/note= "His replaces Ser in wild-type hMnSOD"
FT	FT		
FT	Active-site	58	/note= "His-30"
FT	FT		
FT	Active-site	98	/note= "Tyr-58"
FT	FT		
FT	Active-site	155	/note= "Tyr-74"
FT	Misc-difference	155	/note= "Tyr-74"
FT	FT		
FT	FT		
FT	Active-site	167	/label= Gln, Glu
FT	FT		
FT	Active-site	183	/note= "Gln-143"
FT	FT		
FT	Active-site	185	/note= "Asp-159"
FT	FT		
FT	Active-site	187	/note= "Trp-161"
FT	FT		
FT	Active-site		/note= "His-163"
XX	XX		
PN	WO9913088-A1.		
XX	PN		
XX	18-MAR-1999.		
XX	XX		
PF	10-SEP-1998;	98WO-US018842.	
XX	XX		
PR	10-SEP-1997;	97US-00927230.	
XX	XX		
XX	(UYFL) UNIV FLORIDA.		
XX	XX		
PI	Nick HS, Silverman DN;		
XX	XX		
XX	WPI; 1999-229242/19.		
DR	XX		
XX	XX		
XX	New recombinant human manganese superoxide dismutase proteins.		
XX	Claim 33; Page; 61pp; English.		
XX	XX		
CC	This protein is a H308 mutant of human manganese superoxide dismutase		
CC	(hMnSOD, see also AAW99170). Novel modified hMnSOD proteins having		
CC	the catalytic activity which differs from natural hMnSOD proteins claimed. The		
CC	modified proteins (see also AAW99172-77) exhibit reduced or no product		
CC	inhibition, or have greater activity, or both, compared to natural		
CC	hMnSOD. The modifications involve one or amino acid substitutions within		
CC	the active site of the enzyme, especially at residues His-26, His-30, Tyr		
CC	-34, His-74, Gln-143, Asp-159, Trp-161 and His-163. Gln-143, Tyr-34 and		
CC	His-30 are located near the active site metal, are highly conserved, and		
CC	are involved in a hydrogen bond relay which links the active site metal-		
CC	bound hydroxyl group to ordered solvent, and are thus all potentially		
CC	involved in catalytic activity, product inhibition and/or enzyme		
CC	stability. Modified hMnSODs, or expression vectors in which a modified		
CC	hMnSOD nucleic acid is linked to a promoter (preferably mammalian), are		
CC	used to protect a cell line from damage caused by superoxide radicals		
CC	(claimed). They can also be used to treat subjects suffering from, or at		
CC	risk of, cytotoxicity caused by superoxide radicals (claimed). As such,		
CC	they can be used as antioxidants in the treatment of a variety of		
CC	disorders, including inflammation (claimed), reperfusion injury following		
CC	ischemia (claimed), and cellular damage caused by chemotherapeutic		
CC	agents. Note. The present sequence is not shown in the specification but		
CC	is derived from the hMnSOD sequence given on page 53-54		
XX	Sequence 222 AA;		
SO	SO		

RESULT 30	
AAW98175	
ID	AAW98175 standard; protein; 222 AA.
XX	
AC	AAW98175;
XX	
DT	05-JUL-1999 (first entry)
XX	
DE	Human manganese superoxide dismutase Q143E mutant.
XX	
KW	Superoxide dismutase; MnSOD; SOD; human; protein engineering;
KW	enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
KW	inflammation; reperfusion injury; therapy; mutant.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key
FT	Peptide
FT	1...24 "signal peptide"
FT	25..222
FT	Protein
FT	/note= "mature protein"
FT	50
FT	Active-site
FT	/note= "His-26"
FT	54
FT	Active-site
FT	/note= "His-30"
FT	58
FT	Active-site
FT	/note= "Tyr-58"
FT	98
FT	Active-site
FT	/note= "Tyr-74"
FT	155
FT	Misc-difference
FT	/label= Gln, Glu
FT	167
FT	Misc-difference
FT	/note= "Gln replaces Glu in wild-type hMnSOD"
FT	167
FT	Active-site
FT	/note= "Gln-143"
FT	183
FT	Active-site
FT	/note= "Asp-159"
FT	185
FT	Active-site
FT	/note= "Trp-161"
FT	187
FT	Active-site
FT	/note= "His-163"
XX	
EN	W09913088-A1.
XX	
PD	18-MAR-1999.
XX	
PF	10-SEP-1998; 98WO-US018842.
XX	
PR	10-SEP-1997; 97US-00927230.
XX	
PA	(UYFL) UNIV FLORIDA.
XX	
PI	Nick HS, Silverman DN;
XX	
XX	WPI; 1999-229242/19.
DR	
XX	
PT	New recombinant human manganese superoxide dismutase proteins.
XX	
PS	Claim 14; Page; 6ipp; English.
XX	
CC	This protein is a Q143E mutant of human manganese superoxide dis-
CC	(hMnSOD, see also AAW98170). Novel modified hMnSOD proteins have
CC	catalytic activity which differs from natural hMnSOD are claimed
CC	modified proteins (see also AAW98171-77) exhibit reduced or no p-
CC	inhibition, or have greater activity, or both, compared to natu-
CC	hMnSOD. The modifications involve one or amino acid substitution
CC	the active site of the enzyme, especially at residues His-26, His-
CC	-34, His-74, Gln-143, Asp-159, Trp-161 and His-163. Gln-143, Tyr-
CC	His-30 are located near the active site metal, are highly conse-
CC	are involved in a hydrogen bond relay which links the active sil-
CC	bound hydroxyl group to ordered solvent, and are thus all poten-

Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KYSLPDLYEFSATEPYISQINEIXYT 28
 Db 25 KHSPLDLYDYGALPHINAQIMQLHHS 52

RESULT 34

AAW98174
 ID AAW98174 standard; protein; 222 AA.

AC AAW98174;

XX 05-JUL-1999 (first entry)

XX Human manganese superoxide dismutase Q143D mutant.

XX Superoxide dismutase; MnSOD; SOD; human; protein engineering;
 KW enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
 KW inflammation; reperfusion injury; therapy; mutant.

XX Homo sapiens.

XX Synthetic.

PH Key Location/Qualifiers

FT Peptide 1..24

FT /note= "signal peptide"

FT Protein 25..222

FT /note= "mature protein"

FT Active-site 50

FT /note= "His-26"

FT Active-site 54

FT /note= "His-30"

FT Active-site 58

FT /note= "Tyr-58"

FT Active-site 98

FT /note= "Tyr-74"

FT Misc-difference 155

FT /label= Gln, Glu

FT Misc-difference 167

FT /note= "Gln replaces Asp in wild-type hMnSOD"

FT Active-site 167

FT /note= "Gln-143"

FT Active-site 183

FT /note= "Asp-159"

FT Active-site 185

FT /note= "Trp-161"

FT Active-site 187

FT /note= "His-163"

FT WO9913088-A1.

PN 18-MAR-1999.

XX 10-SEP-1998; 98WO-US018842.

XX 10-SEP-1997; 97US-00927230.

XX (UYFL) UNIV FLORIDA.

XX Nick HS, Silverman DN;

XX WPI; 1999-229242/19.

XX New recombinant human manganese superoxide dismutase proteins.

XX Claim 14; Page; 61pp; English.

XX This protein is a Q143D mutant of human manganese superoxide dismutase

CC (hMnSOD, see also AAW98170). Novel modified hMnSOD proteins having

CC catalytic activity which differs from natural hMnSOD are claimed. The

CC modified proteins (see also AAW98171-77) exhibit reduced or no product

CC inhibition, or have greater activity, or both, compared to natural

CC hMnSOD. The modifications involve one or amino acid substitutions within
 CC the active site of the enzyme, especially at residues His-26, His-30, Tyr
 CC -34, His-74, Gln-143, Asp-159, Trp-161 and His-163. Gln-143, Tyr-34 and
 CC His-30 are located near the active site metal, are highly conserved, and
 CC are involved in a hydrogen bond relay which links the active site metal-
 CC bound hydroxyl group to ordered solvent, and are thus all potentially
 CC involved in catalytic activity, product inhibition and/or enzyme
 CC stability. Modified hMnSODs, or expression vectors in which a modified
 CC hMnSOD nucleic acid is linked to a promoter (preferably mammalian), are
 CC used to protect a cell line from damage caused by superoxide radicals
 CC (claimed). They can also be used to treat subjects suffering from, or at
 CC risk of, cytotoxicity caused by superoxide radicals (claimed). As such,
 CC they can be used as antioxidants in the treatment of a variety of
 CC disorders, including inflammation (claimed), reperfusion injury following
 CC ischemia (claimed), and cellular damage caused by chemotherapeutic
 CC agents. Note. The present sequence is not shown in the specification but
 CC is derived from the hMnSOD sequence given on page 53-54
 XX Sequence 222 AA;

Query Match 51.0%; Score 74; DB 2; Length 222;
 Best Local Similarity 42.9%; Pred. No. 0.0011;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KYSLPDLYEFSATEPYISQINEIXYT 28

Db 25 KHSPLDLYDYGALPHINAQIMQLHHS 52

RESULT 35

AAW98169

ID AAW98169 standard; protein; 222 AA.

XX AAW98169;

XX 05-JUL-1999 (first entry)

XX Human native manganese superoxide dismutase.

XX Superoxide dismutase; MnSOD; SOD; human; protein engineering;
 KW enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
 KW inflammation; reperfusion injury; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..24

FT /note= "signal peptide"

FT Protein 25..222

FT /note= "mature protein"

FT Active-site 50

FT /note= "His-26"

FT Active-site 54

FT /note= "His-30"

FT Active-site 58

FT /note= "Tyr-58"

FT Active-site 98

FT /note= "Tyr-74"

FT Active-site 167

FT /note= "Gln-143"

FT Active-site 183

FT /note= "Asp-159"

FT Active-site 185

FT /note= "Trp-161"

FT Active-site 187

FT /note= "His-163"

XX WO9913088-A1.

XX 18-MAR-1999.

XX 10-SEP-1998; 98WO-US018842.

PR 10-SEP-1997; 97US-00927230.
 XX (UYFL) UNIV FLORIDA.
 XX
 PA Nick HS, Silverman DN;
 XX
 PI WPI; 1999-229242/19.
 XX N-PSDB; AAX24998.
 XX
 DR New recombinant human manganese superoxide dismutase proteins.
 XX
 PT Disclosure; Page 52-53; 61pp; English.
 XX
 PS This protein is human manganese superoxide dismutase (hMnSOD). Novel
 XX hMnSOD proteins having catalytic activity which differs from this natural
 CC hMnSOD are claimed (see AAW98171-77). The modified proteins exhibit
 CC reduced or no product inhibition, or have greater activity, or both,
 CC compared to natural hMnSOD. The modifications involve one or amino acid
 CC substitutions within the active site of the enzyme, especially at
 CC residues His-26, His-30, Tyr-34, His-74, Gln-143, Asp-159, Trp-161 and
 CC His-163. The modified hMnSOD, or expression vectors in which modified
 CC hMnSOD nucleic acid is linked to a promoter (preferably mammalian), can
 CC be used to protect a cell line from damage caused by superoxide radicals
 CC (claimed). They can also be used to treat subjects suffering from, or at
 CC risk of, cytotoxicity caused by superoxide radicals (claimed). As such,
 CC they can be used as antioxidants in the treatment of a variety of
 CC disorders, including inflammation (claimed), reperfusion injury following
 CC ischemia (claimed), and cellular damage caused by chemotherapeutic agents
 XX
 SQ Sequence 222 AA;
 Query Match 51.0%; Score 74; DB 2; Length 222;
 Best Local Similarity 42.9%; Pred. No. 0.0011;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
 QY 1 KYSLPELDYFSATEPYISQINEIXYT 28
 DB 25 KHSLEPDLFYDYGALPEHINAQIMQLHHS 52
 RESULT 36
 AAW98173
 ID AAW98173 standard; protein; 222 AA.
 AC AAW98173;
 XX
 XX 05-JUL-1999 (first entry)
 DT
 XX Human manganese superoxide dismutase Q143H mutant.
 DE
 XX Superoxide dismutase; MnSOD; SOD; human; protein engineering;
 KW enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
 KW inflammation; reperfusion injury; therapy; mutant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH 1..24
 FT Peptide /note= "signal peptide"
 FT Protein /note= "mature protein"
 FT Active-site 50
 FT Active-site 54 /note= "His-26"
 FT Active-site 58 /note= "His-30"
 FT Active-site 58 /note= "Tyr-58"
 FT Active-site 98 /note= "Tyr-74"
 FT Misc-difference 155
 FT /label= Gln, Glu
 FT Misc-difference 167

FT Active-site 167 /note= "Gln replaces His in wild-type hMnSOD"
 FT 183 /note= "Gln-143"
 FT Active-site 185 /note= "Asp-159"
 FT Active-site 187 /note= "Trp-161"
 FT 187 /note= "His-163"
 XX
 PN WO9913088-A1.
 XX
 PD 18-MAR-1999.
 XX
 XX 10-SEP-1998; 98WO-US018842.
 PF
 XX 10-SEP-1997; 97US-00927230.
 PR (UYFL) UNIV FLORIDA.
 XX
 PA Nick HS, Silverman DN;
 XX
 PI WPI; 1999-229242/19.
 XX
 DR New recombinant human manganese superoxide dismutase proteins.
 XX
 PT Claim 14; Page; 61pp; English.
 PS
 XX This protein is a Q143H mutant of human manganese superoxide dismutase
 CC (hMnSOD, see also AAW98170). Novel modified hMnSOD proteins having
 CC catalytic activity which differs from natural hMnSOD are claimed. The
 CC modified proteins (see also AAW98171-77) exhibit reduced or no product
 CC inhibition, or have greater activity, or both, compared to natural
 CC hMnSOD. The modifications involve one or amino acid substitutions within
 CC the active site of the enzyme, especially at residues His-26, His-30, Tyr
 CC -34, His-74, Gln-143, Asp-159, Trp-161 and His-163. Gln-143, Tyr-34 and
 CC His-30 are located near the active site metal, are highly conserved, and
 CC are involved in a hydrogen bond relay which links the active site metal-
 CC bound hydroxyl group to ordered solvent, and are thus all potentially
 CC involved in catalytic activity, product inhibition and/or enzyme
 CC stability. Modified hMnSODs, or expression vectors in which a modified
 CC hMnSOD nucleic acid is linked to a promoter (preferably mammalian), are
 CC used to protect a cell line from damage caused by superoxide radicals
 CC (claimed). They can also be used to treat subjects suffering from, or at
 CC risk of, cytotoxicity caused by superoxide radicals (claimed). As such,
 CC they can be used as antioxidants in the treatment of a variety of
 CC disorders, including inflammation (claimed), reperfusion injury following
 CC ischemia (claimed), and cellular damage caused by chemotherapeutic
 CC agents. Note. The present sequence is not shown in the specification but
 CC is derived from the hMnSOD sequence given on page 53-54
 XX
 SQ Sequence 222 AA;
 Query Match 51.0%; Score 74; DB 2; Length 222;
 Best Local Similarity 42.9%; Pred. No. 0.0011;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
 QY 1 KYSLPELDYFSATEPYISQINEIXYT 28
 DB 25 KHSLEPDLFYDYGALPEHINAQIMQLHHS 52
 RESULT 37
 AAW98176
 ID AAW98176 standard; protein; 222 AA.
 AC AAW98176;
 XX
 XX 05-JUL-1999 (first entry)
 DT
 XX Human manganese superoxide dismutase H30N mutant.
 DE
 XX Superoxide dismutase; MnSOD; SOD; human; protein engineering;
 KW

QY
1 KYSLPDYEFSA TE PYISGQINEIXYT 28

QY
1 KYSLPELDYEFSATEPYISGQINEIXYT 28
 | : | : | : | : | : | : | : | :
25 KHSIPDIPYDYGALEPHINAQIMOLHHS 52

Thu Sep 2 12:32:51 2004

us-09-987-190-2.rag

Page 21

Search completed: August 24, 2004, 23:00:36
Job time : 126 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 24, 2004, 22:58:32 ; Search time 31 Seconds
(without alignments)
49.961 Million cell updates/sec

Title: US-09-987-190-2

Perfect score: 145

Sequence: 1 KYSLPELDYEFSAPEYISGQINEIXYXX 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
 - 2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
 - 3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
 - 4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
 - 5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep.*
 - 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	141	97.2	30	4	US-09-262-856A-2
2	103	71.0	207	4	US-09-214-909-24
3	100	69.0	233	2	US-08-928-692-31
4	100	69.0	233	4	US-09-339-972-31
5	79	54.5	30	4	US-09-091-097-52
6	79	54.5	224	4	US-09-091-097-8
7	77	53.1	200	4	US-09-373-731-2
8	74	51.0	198	3	US-09-075-019-2
9	74	51.0	198	6	5240847-11
10	74	51.0	198	6	5240847-11
11	74	51.0	222	2	US-08-365-486A-28
12	74	51.0	222	2	US-08-023-980B-44
13	74	51.0	222	2	US-08-486-953A-52
14	74	51.0	222	2	US-08-927-230A-2
15	74	51.0	222	2	US-08-927-230A-3
16	74	51.0	222	3	US-09-151-052-2
17	74	51.0	222	3	US-09-151-052-3
18	74	51.0	222	3	US-09-126-109-2
19	74	51.0	222	3	US-08-880-342-28
20	74	51.0	226	3	US-09-075-019-7
21	71	49.0	188	4	US-09-262-856A-6
22	70	48.3	46	6	5240847-24
23	70	48.3	214	4	US-09-198-452A-75
24	69	47.6	230	2	US-08-928-692-30
25	69	47.6	230	4	US-09-339-972-30
26	66	45.5	22	4	US-09-157-689-23
27	63	43.4	217	4	US-09-489-039A-1227

28	62	42.8	206	4	US-09-091-097-6
29	58	40.0	214	3	US-09-411-578-1
30	58	40.0	214	4	US-09-749-233-1
31	58	40.0	224	4	US-09-543-681A-6654
32	58	40.0	241	4	US-09-540-236-3442
33	57	39.3	201	4	US-09-134-001C-3584
34	56	38.6	190	4	US-08-679-493A-184
35	55	37.9	205	4	US-09-543-681A-4456
36	54	37.2	245	4	US-09-252-991A-24333
37	53	36.6	204	1	US-08-445-909A-17
38	53	36.6	204	1	US-08-445-909A-29
39	52	35.9	207	4	US-09-252-991A-24593
40	50	34.5	371	4	US-09-636-215-708
41	50	34.5	371	4	US-09-685-166A-708
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44	50	34.5	553	3	US-09-020-956-113
45	50	34.5	553	3	US-09-030-607-113

ALIGNMENTS

RESULT 1

US-09-262-856A-2
; Sequence 2, Application US/09262856A
; Patent No. 633164

GENERAL INFORMATION:
; APPLICANT: TAKESAKO, Kazutoh

; APPLICANT: MIZUTANI, Shigetoshi

; APPLICANT: ENDO, Masahiro

; APPLICANT: KATO, Ikunoshin

; TITLE OF INVENTION: FUNGAL ANTIGENS AND PROCESS FOR PRODUCING THE SAME

; FILE REFERENCE: 1422-372P

; CURRENT APPLICATION NUMBER: US/09/262,856A

; CURRENT FILING DATE: 1999-03-04

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 30

; TYPE: PRT

; ORGANISM: Candida albicans

; FEATURE:

; OTHER INFORMATION: residues 26, 39, 30 = unknown

US-09-262-856A-2

Query Match 97.2%; Score 141; DB 4; Length 30;

Best Local Similarity 100.0%; Pred No. 1.6e-16;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSAPEYISGQINEIXYT 28

Db 1 KYSLPELDYEFSAPEYISGQINEIXYT 28

RESULT 2

US-09-214-909-24

; Sequence 24, Application US/09214909

; Patent No. 6486382

GENERAL INFORMATION:

; APPLICANT: GORDON-KAMM, WILLIAM

; APPLICANT: PIERCE, DOROTHY A.

; APPLICANT: BOWEN, BENJAMIN

; APPLICANT: BIDNEY, DENNIS

; APPLICANT: ROSS, MARGIT

; APPLICANT: SCELONGE, CHRISTOPHER

; APPLICANT: MILLER, MICHAEL D.

; APPLICANT: SANDAHL, GARY

; APPLICANT: WANG, LIJUAN

; TITLE OF INVENTION: USE OF THE GREEN FLUORESCENT PROTEIN AS A SCREENABLE

; FILE REFERENCE: 03329/0682

; CURRENT APPLICATION NUMBER: US/09/214,909

QY	1	KYSLPELDYEFSAPEYISGQINEIXYT	28
DB	27	KVTLPDLKWDGFALEPYISGQINELHVT	54
<p>US-09-339-972-31</p> <p>Sequence 31, Application US/09339972</p> <p>Patent No. 6323002</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Brody, Howard</p> <p>APPLICANT: Yaver, Deborah S.</p> <p>APPLICANT: Lamsa, Michael</p> <p>APPLICANT: Hansen, Kim</p> <p>TITLE OF INVENTION: Methods for Modifying the Production of</p> <p>TITLE OF INVENTION: a Polypeptide</p> <p>NUMBER OF SEQUENCES: 80</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: No. 63230020 No. 6323002disk of No. 6323002th America, Inc.</p> <p>STREET: 405 Lexington Avenue</p> <p>CITY: New York</p> <p>STATE: NY</p> <p>COUNTRY: USA</p> <p>ZIP: 10174</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Diskette</p> <p>COMPUTER: IBM Compatible</p> <p>OPERATING SYSTEM: DOS</p> <p>SOFTWARE: FastSEQ for Windows Version 2.0</p> <p>CURRENT APPLICATION DATA: US/09/339,972</p> <p>FILING DATE:</p> <p>CLASSIFICATION:</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: 08/928,692</p> <p>FILING DATE:</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Lambiris, Elias J</p> <p>REGISTRATION NUMBER: 33,728</p> <p>REFERENCE/DOCKET NUMBER: 4944.200-US</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 212-867-0123</p> <p>TELEFAX: 212-878-9655</p> <p>INFORMATION FOR SEQ ID NO: 31:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 233 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: No. 6323002e</p> <p>US-09-339-972-31</p>			
QY	1	KYSLPELDYEFSAPEYISGQINEIXYT	28
DB	27	KVTLPDLKWDGFALEPYISGQINELHVT	54
<p>US-09-339-972-31</p> <p>Sequence 31, Application US/09339972</p> <p>Patent No. 6323002</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Brody, Howard</p> <p>APPLICANT: Yaver, Deborah S.</p> <p>APPLICANT: Lamsa, Michael</p> <p>APPLICANT: Hansen, Kim</p> <p>TITLE OF INVENTION: Methods for Modifying the Production of</p> <p>TITLE OF INVENTION: a Polypeptide</p> <p>NUMBER OF SEQUENCES: 80</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: No. 63230020 No. 6323002disk of No. 6323002th America, Inc.</p> <p>STREET: 405 Lexington Avenue</p> <p>CITY: New York</p> <p>STATE: NY</p> <p>COUNTRY: USA</p> <p>ZIP: 10174</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Diskette</p> <p>COMPUTER: IBM Compatible</p> <p>OPERATING SYSTEM: DOS</p> <p>SOFTWARE: FastSEQ for Windows Version 2.0</p> <p>CURRENT APPLICATION DATA: US/09/339,972</p> <p>FILING DATE:</p> <p>CLASSIFICATION:</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: 08/928,692</p> <p>FILING DATE:</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Lambiris, Elias J</p> <p>REGISTRATION NUMBER: 33,728</p> <p>REFERENCE/DOCKET NUMBER: 4944.200-US</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 212-867-0123</p> <p>TELEFAX: 212-878-9655</p> <p>INFORMATION FOR SEQ ID NO: 31:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 233 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: No. 6323002e</p> <p>US-09-339-972-31</p>			
QY	1	KYSLPELDYEFSAPEYISGQINEIXYT	28
DB	27	KVTLPDLKWDGFALEPYISGQINELHVT	54
<p>US-09-339-972-31</p> <p>Sequence 31, Application US/09339972</p> <p>Patent No. 6323002</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Brody, Howard</p> <p>APPLICANT: Yaver, Deborah S.</p> <p>APPLICANT: Lamsa, Michael</p> <p>APPLICANT: Hansen, Kim</p> <p>TITLE OF INVENTION: Methods for Modifying the Production of</p> <p>TITLE OF INVENTION: a Polypeptide</p> <p>NUMBER OF SEQUENCES: 80</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: No. 63230020 No. 6323002disk of No. 6323002th America, Inc.</p> <p>STREET: 405 Lexington Avenue</p> <p>CITY: New York</p> <p>STATE: NY</p> <p>COUNTRY: USA</p> <p>ZIP: 10174</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Diskette</p> <p>COMPUTER: IBM Compatible</p> <p>OPERATING SYSTEM: DOS</p> <p>SOFTWARE: FastSEQ for Windows Version 2.0</p> <p>CURRENT APPLICATION DATA: US/09/339,972</p> <p>FILING DATE:</p> <p>CLASSIFICATION:</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: 08/928,692</p> <p>FILING DATE:</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Lambiris, Elias J</p> <p>REGISTRATION NUMBER: 33,728</p> <p>REFERENCE/DOCKET NUMBER: 4944.200-US</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 212-867-0123</p> <p>TELEFAX: 212-878-9655</p> <p>INFORMATION FOR SEQ ID NO: 31:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 233 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: No. 6323002e</p> <p>US-09-339-972-31</p>			
QY	1	KYSLPELDYEFSAPEYISGQINEIXYT	28
DB	27	KVTLPDLKWDGFALEPYISGQINELHVT	54
<p>US-09-339-972-31</p> <p>Sequence 31, Application US/09339972</p> <p>Patent No. 6323002</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Brody, Howard</p> <p>APPLICANT: Yaver, Deborah S.</p> <p>APPLICANT: Lamsa, Michael</p> <p>APPLICANT: Hansen, Kim</p> <p>TITLE OF INVENTION: Methods for Modifying the Production of</p> <p>TITLE OF INVENTION: a Polypeptide</p> <p>NUMBER OF SEQUENCES: 80</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: No. 63230020 No. 6323002disk of No. 6323002th America, Inc.</p> <p>STREET: 405 Lexington Avenue</p> <p>CITY: New York</p> <p>STATE: NY</p> <p>COUNTRY: USA</p> <p>ZIP: 10174</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Diskette</p> <p>COMPUTER: IBM Compatible</p> <p>OPERATING SYSTEM: DOS</p> <p>SOFTWARE: FastSEQ for Windows Version 2.0</p> <p>CURRENT APPLICATION DATA: US/09/339,972</p> <p>FILING DATE:</p> <p>CLASSIFICATION:</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: 08/928,692</p> <p>FILING DATE:</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Lambiris, Elias J</p> <p>REGISTRATION NUMBER: 33,728</p> <p>REFERENCE/DOCKET NUMBER: 4944.200-US</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 212-867-0123</p> <p>TELEFAX: 212-878-9655</p> <p>INFORMATION FOR SEQ ID NO: 31:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 233 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: No. 6323002e</p> <p>US-09-339-972-31</p>			
QY	1	KYSLPELDYEFSAPEYISGQINEIXYT	28
DB	27	KVTLPDLKWDGFALEPYISGQINELHVT	54
<p>US-09-339-972-31</p> <p>Sequence 31, Application US/09339972</p> <p>Patent No. 6323002</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Brody, Howard</p> <p>APPLICANT: Yaver, Deborah S.</p> <p>APPLICANT: Lamsa, Michael</p> <p>APPLICANT: Hansen, Kim</p> <p>TITLE OF INVENTION: Methods for Modifying the Production of</p> <p>TITLE OF INVENTION: a Polypeptide</p> <p>NUMBER OF SEQUENCES: 80</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: No. 63230020 No. 6323002disk of No. 6323002th America, Inc.</p> <p>STREET: 405 Lexington Avenue</p> <p>CITY: New York</p> <p>STATE: NY</p> <p>COUNTRY: USA</p> <p>ZIP: 10174</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Diskette</p> <p>COMPUTER: IBM Compatible</p> <p>OPERATING SYSTEM: DOS</p> <p>SOFTWARE: FastSEQ for Windows Version 2.0</p> <p>CURRENT APPLICATION DATA: US/09/339,972</p> <p>FILING DATE:</p> <p>CLASSIFICATION:</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: 08/928,692</p> <p>FILING DATE:</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Lambiris, Elias J</p> <p>REGISTRATION NUMBER: 33,728</p> <p>REFERENCE/DOCKET NUMBER: 4944.200-US</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 212-867-0123</p> <p>TELEFAX: 212-878-9655</p> <p>INFORMATION FOR SEQ ID NO: 31:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 233 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: No. 6323002e</p> <p>US-09-339-972-31</p>			
QY	1	KYSLPELDYEFSAPEYISGQINEIXYT	28
DB	27	KVTLPDLKWDGFALEPYISGQINELHVT	54
<p>US-09-339-972-31</p> <p>Sequence 31, Application US/09339972</p> <p>Patent No. 6323002</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Brody, Howard</p> <p>APPLICANT: Yaver, Deborah S.</p>			

APPLICANT: YASUEDA, HIROSHI
APPLICANT: YAMAGUCHI, HIDEYO
TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
TITLE OF INVENTION: MALASSEZIA
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,097
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422-0346P
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-091-097-52

Query Match 54.5%; Score 79; DB 4; Length 30;
Best Local Similarity 55.6%; Pred. No. 2.8e-06;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSSATEPYISQINEIYY 27
DB 1 KYTLPLPDYDYGALPAISGEINETHY 27

RESULT 6

US-09-091-097-8
Sequence 8, Application US/09091097
Patent No. 6432407
GENERAL INFORMATION:
APPLICANT: TAKESAKO, KAZUTOH
APPLICANT: OKADO, TAKASHI
APPLICANT: YAGIHARA, TOMOKO
APPLICANT: KURODA, MASANOBU
APPLICANT: ONISHI, YOSHIMI
APPLICANT: KATO, IKUNOSHIN
APPLICANT: AKIYAMA, KAZUO
APPLICANT: YASUEDA, HIROSHI
APPLICANT: YAMAGUCHI, HIDEYO
TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
TITLE OF INVENTION: MALASSEZIA
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,097
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422-0346P
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-091-097-8

Query Match 54.5%; Score 79; DB 4; Length 224;
Best Local Similarity 55.6%; Pred. No. 3.8e-05;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSSATEPYISQINEIYY 27
DB 25 KYTLPLPDYDYGALPAISGEINETHY 51

RESULT 7

US-09-373-731-2
Sequence 2, Application US/09373731
Patent No. 6589650
GENERAL INFORMATION:
APPLICANT: DEGUSSA-HULS AG
APPLICANT: CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
TITLE OF INVENTION: A PROCESS FOR THE FERMENTATIVE PREPARATION OF METABOLIC
TITLE OF INVENTION: PRODUCTS AND FOR THE NUCLEOTIDE SEQUENCES ENCODING FOR
TITLE OF INVENTION: THE SOD GENE
FILE REFERENCE: MERKAMM
CURRENT APPLICATION NUMBER: US/09/373,731
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 200
TYPE: PRT
ORGANISM: Corynebacterium melassecola
US-09-373-731-2

Query Match 53.1%; Score 77; DB 4; Length 200;
Best Local Similarity 48.1%; Pred. No. 7e-05;
Matches 13; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSSATEPYISQINEIYYT 28
DB 4 YELPELDYDALEPHIAEIMELHHS 30

RESULT 8

US-09-075-019-2
Sequence 2, Application US/09075019
Patent No. 6190658
GENERAL INFORMATION:
APPLICANT: UTC IR459
TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
TITLE OF INVENTION: SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: CO

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Clark & Elbing LLP
;; STREET: 585 Commercial Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02109-1024
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/023,980B
;; FILING DATE: 26-FEB-1993
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Clark, Paul T.
;; REGISTRATION NUMBER: 30,162
;; REFERENCE/DOCKET NUMBER: 00786/177001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/723-4123
;; TELEFAX: 617/723-8962
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 44:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 222 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-023-980B-44

Query Match 51.0%; Score 74; DB 2; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.00025;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDLYEFSATEPYISQINEIXYT 28
Db 25 KHSPLDLPYDYGALPHINAQIMQLHHS 52

RESULT 13
US-08-486-953A-52
; Sequence 52, Application US/08486953A
; Patent No. 5849290
; GENERAL INFORMATION:
; APPLICANT: Brown, Robert
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Rosen, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
; TREATMENT AND PREVENTION OF DISEASES OF CELL DEATH
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,953A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/204,052
; FILING DATE: 28-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.

;; REGISTRATION NUMBER: 30,162
;; REFERENCE/DOCKET NUMBER: 00786/223002
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/428-0200
;; TELEFAX: 617/428-7045
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 52:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 222 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-486-953A-52

Query Match 51.0%; Score 74; DB 2; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.00025;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDLYEFSATEPYISQINEIXYT 28
Db 25 KHSPLDLPYDYGALPHINAQIMQLHHS 52

RESULT 14
US-08-927-230A-2
; Sequence 2, Application US/08927230A
; Patent No. 5985633
; GENERAL INFORMATION:
; APPLICANT: Nick et al.
; TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street, Floor 24
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,230A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: UFJ-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 131
; OTHER INFORMATION: Xaa can code for Gln or Glu
; US-08-927-230A-2

Query Match 51.0%; Score 74; DB 2; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.00025;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDLYEFSATEPYISQINEIXYT 28
 Db 25 KHSPLDLYDYGALPHINAQIMQLHHS 52

RESULT 15

US-08-927-230A-3
 ; Sequence 3, Application US/08927230A
 ; Patent No. 5985633
 ; GENERAL INFORMATION:
 ; APPLICANT: Nick et al.
 ; TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street, Floor 24
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/927,230A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Remillard, Jane
 ; REGISTRATION NUMBER: 38,872
 ; REFERENCE/DOCKET NUMBER: UFJ-001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)742-4214
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 222 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: OTHER
 ; LOCATION: 131
 ; OTHER INFORMATION: Xaa can code for Gln or Glu

US-08-927-230A-3
 Query Match 51.0%; Score 74; DB 2; Length 222;
 Best Local Similarity 42.9%; Pred. No. 0.00025;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDLYEFSATEPYISQINEIXYT 28
 Db 25 KHSPLDLYDYGALPHINAQIMQLHHS 52

RESULT 16

US-09-151-052-2
 ; Sequence 2, Application US/09151052
 ; Patent No. 6107070
 ; GENERAL INFORMATION:
 ; APPLICANT: Nick et al.
 ; TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 28 State Street, Floor 24
 ; CITY: Boston
 ; STATE: Massachusetts

; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/151,052
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/927,230
 ; FILING DATE: September 10, 1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Remillard, Jane
 ; REGISTRATION NUMBER: 38,872
 ; REFERENCE/DOCKET NUMBER: UFJ-001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)742-4214
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 222 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: OTHER
 ; LOCATION: 131
 ; OTHER INFORMATION: Xaa can code for Gln or Glu

US-09-151-052-2
 Query Match 51.0%; Score 74; DB 3; Length 222;
 Best Local Similarity 42.9%; Pred. No. 0.00025;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDLYEFSATEPYISQINEIXYT 28
 Db 25 KHSPLDLYDYGALPHINAQIMQLHHS 52

RESULT 17

US-09-151-052-3
 ; Sequence 3, Application US/09151052
 ; Patent No. 6107070
 ; GENERAL INFORMATION:
 ; APPLICANT: Nick et al.
 ; TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 28 State Street, Floor 24
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/151,052
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/927,230
 ; FILING DATE: September 10, 1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Remillard, Jane
 ; REGISTRATION NUMBER: 38,872
 ; REFERENCE/DOCKET NUMBER: UFJ-001

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 131
; OTHER INFORMATION: Xaa can code for Gln or Glu
US-09-151-052-3

Query Match 51.0%; Score 74; DB 3; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.00025;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDLYEFSATEPYISGQINEIXYT 28
Db 25 KHSLPDLPDYGALEPHINAQIMQLHHS 52

RESULT 18
US-09-126-109-2
; Sequence 2, Application US/09126109
; Patent No. 6171856
; GENERAL INFORMATION:
; APPLICANT: Thigpen, Anice
; APPLICANT: Hohmeier, Hans-Ewald
; APPLICANT: Newgard, Christopher B.
; APPLICANT: Unger, Roger H.
; APPLICANT: Shimabukuro, Michio
; APPLICANT: Chen, Guaxun
; APPLICANT: Rhodes, Christopher J.
; APPLICANT: Hugl, Sigrun R.
; APPLICANT: Cousin, Sharon
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
; TITLE OF INVENTION: TO NO-MEDIATED CYTOTOXICITY
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09126,109
; FILING DATE: 30-JUL-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/055,092
; FILING DATE: 30-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US Unknown
; FILING DATE: 03-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: McMillian, Nabeela R.
; REGISTRATION NUMBER: P-43,363
; REFERENCE/DOCKET NUMBER: UTSD:560
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
```

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;
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-126-109-2

Query Match 51.0%; Score 74; DB 3; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.00025;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDLYEFSATEPYISGQINEIXYT 28
Db 25 KHSLPDLPDYGALEPHINAQIMQLHHS 52

RESULT 19
US-08-880-342-28
; Sequence 28, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,342
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB95/00996
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/365,486
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-880-342-28

Query Match 51.0%; Score 74; DB 3; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.00025;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDLYEFSATEPYISGQINEIXYT 28
Db 25 KHSLPDLPDYGALEPHINAQIMQLHHS 52
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Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 13 ATEPYISGQINEIXYT 28
      |||||:|||||
Db 1 ATEPYITGQNEIHYT 16

RESULT 22
5240847-24
Patent No. 5240847
; APPLICANT: HECKL, KONRAD; SPEVAK, WALTER; OSTERMANN, ELINBORG;
; ZOPHEL, ANDREAS; KRISTEK, EDELTRAUD; MAURER-FOGY, INGRID;
; WICHE-CASTANON, MARIA J.; STRATONA, CHRISTIAN; HAUTMANN, RUDOLF
; TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
; (HMN-SOD)
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/167,261
; FILING DATE: 11-MAR-1988
; SEQ ID NO: 24:
; LENGTH: 46
5240847-24

Query Match 48.3%; Score 70; DB 6; Length 46;
Best Local Similarity 54.3%; Pred. No. 0.00015;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
QY 1 KYSLPDLYEFSATEPYISGQI 22
      :|||:|:|:|:|:|
Db 25 KHSLPDLPYDYGALPEHNAQI 46

RESULT 23
US-09-198-452A-75
; Sequence 75, Application US/09198452A
; Patent No. 6553294
; GENERAL INFORMATION:
; APPLICANT: Griffls, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides,
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 75
; LENGTH: 214
; TYPE: PRF
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-75

Query Match 48.3%; Score 70; DB 4; Length 214;
Best Local Similarity 61.9%; Pred. No. 0.0011;
Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 2 YSLPDLDFEFSATEPYISGQI 22
      |||||:|:|:|:|
Db 13 YSLPDLFYDYDALEPVISSEI 33

RESULT 24
US-08-928-692-30
; Sequence 30, Application US/08928692
; Patent No. 5958727
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Yaver, Deborah S.
; APPLICANT: Lamer, Michael
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; TITLE OF INVENTION: a polypeptide
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:

```

```
;
; ADDRESSEE: No. 5958727o No. 5958727disk of No. 5958727th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,692
; FILING DATE: 12-SEPT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5958727e
; US-08-928-692-30

Query Match 47.6%; Score 69; DB 2; Length 230;
Best Local Similarity 48.1%; Pred. No. 0.0018;
Matches 13; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

;
; QY 1 KYSLPDYEFSTPEYISQINEIXY 27
; Db 36 KATPLDAYDYGALPSISGKIMELHH 62

RESULT 25
US-09-339-972-30
; Sequence 30, Application US/09339972
; Patent No. 6323002
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Yaver, Deborah S.
; APPLICANT: Lamsa, Michael
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; TITLE OF INVENTION: a Polypeptide
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6323002o No. 6323002disk of No. 6323002th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/339,972
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/928,692
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J

;
; QY 1 KYSLPDYEFSTPEYISQINEIXY 27
; Db 36 KATPLDAYDYGALPSISGKIMELHH 62

RESULT 26
US-09-157-689-23
; Sequence 23, Application US/09157689
; Patent No. 6599510
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Marcus A.
; APPLICANT: Harth, Gunter
; TITLE OF INVENTION: Abundant Extracellular Products and
; TITLE OF INVENTION: Methods for Their Production and Use
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kurt A. MacLean
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,689
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/568,357
; FILING DATE: 06-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/551,149
; FILING DATE: 31-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/447,398
; FILING DATE: 23-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,667
; FILING DATE: 12-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/156,358
; FILING DATE: 23-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLean, Kurt A.
; REGISTRATION NUMBER: 31,118
; REFERENCE/DOCKET NUMBER: 118-119
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 277-1297
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
```

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;
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6323002e
; US-09-339-972-30

Query Match 47.6%; Score 69; DB 4; Length 230;
Best Local Similarity 48.1%; Pred. No. 0.0018;
Matches 13; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

;
; QY 1 KYSLPDYEFSTPEYISQINEIXY 27
; Db 36 KATPLDAYDYGALPSISGKIMELHH 62

RESULT 26
US-09-157-689-23
; Sequence 23, Application US/09157689
; Patent No. 6599510
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Marcus A.
; APPLICANT: Harth, Gunter
; TITLE OF INVENTION: Abundant Extracellular Products and
; TITLE OF INVENTION: Methods for Their Production and Use
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kurt A. MacLean
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,689
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/568,357
; FILING DATE: 06-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/551,149
; FILING DATE: 31-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/447,398
; FILING DATE: 23-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,667
; FILING DATE: 12-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/156,358
; FILING DATE: 23-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLean, Kurt A.
; REGISTRATION NUMBER: 31,118
; REFERENCE/DOCKET NUMBER: 118-119
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 277-1297
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
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```

;
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; STRAIN: Erdman
;
US-09-157-689-23

Query Match 45.5%; Score 66; DB 4; Length 22;
Best Local Similarity 61.1%; Pred. No. 0.00026;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 4 LPDLDFEFSATEPYISQ 21
Db 5 LPDLDFEFSATEPYISQ 22

RESULT 27
US-09-489-039A-12227
; Sequence 12227, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12227
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12227

Query Match 43.4%; Score 63; DB 4; Length 217;
Best Local Similarity 44.4%; Pred. No. 0.016;
Matches 12; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 2 YSLPDLDFEFSATEPYISQINEIXYT 28
Db 14 YTLFSLPYDAYDALEPHFDKQTMETHT 40

RESULT 28
US-09-091-097-6
; Sequence 6, Application US/09091097
; Patent No. 6432407
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH
; APPLICANT: OKADO, TAKASHI
; APPLICANT: YAGIHARA, TOMOKO
; APPLICANT: KURODA, MASANOBU
; APPLICANT: ONISHI, YOSHIMI
; APPLICANT: KATO, IKUNOSHIN
; APPLICANT: AKIYAMA, KAZUO
; APPLICANT: YASUEDA, HIROSHI
; APPLICANT: YAMAGUCHI, HIDEYO
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
; TITLE OF INVENTION: MALASSEZIA
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA

;
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/091,097
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-0346P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-091-097-6

Query Match 42.8%; Score 62; DB 4; Length 206;
Best Local Similarity 40.7%; Pred. No. 0.022;
Matches 11; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 KYSLPELDYFESATEPYISQINEIXY 27
Db 6 EYTLPLPYDAYDALEPFISKEIMTVHH 32

RESULT 29
US-09-411-578-1
; Sequence 1, Application US/09411578
; Patent No. 6203801
; GENERAL INFORMATION:
; APPLICANT: Schaap, Theodorus C
; APPLICANT: Kuiper, Catharina M
; APPLICANT: Vermeulen, Arnoldus N
; TITLE OF INVENTION: Coccidiosis Vaccines
; FILE REFERENCE: schaap
; CURRENT APPLICATION NUMBER: US/09/411,578
; CURRENT FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 98203384.7
; EARLIER FILING DATE: 1998-10-07
; EARLIER APPLICATION NUMBER: 98203457.1
; EARLIER FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Eimeria tenella
US-09-411-578-1

Query Match 40.0%; Score 58; DB 3; Length 214;
Best Local Similarity 46.2%; Pred. No. 0.11;
Matches 12; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 2 YSLPELDYFESATEPYISQINEIXY 27
Db 3 FELPPLPYMDALEPFYSKETLEYHY 28

RESULT 30
US-09-749-233-1
; Sequence 1, Application US/09749233
; Patent No. 6680061
; GENERAL INFORMATION:
```


RESULT 35
US-09-543-681A-4456
; Sequence 4456, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4456
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4456
Query Match 37.9%; Score 55; DB 4; Length 205;
Best Local Similarity 42.3%; Pred. No. 0.31;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
QY 2 YSLPELDYFSATPEYISGQINEIXY 27
Db 16 FELPKLPYDALEPHISKETLEYHY 41
RESULT 36
US-09-252-991A-24333
; Sequence 24333, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24333
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24333
Query Match 37.2%; Score 54; DB 4; Length 245;
Best Local Similarity 47.8%; Pred. No. 0.57;
Matches 11; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 2 YSLPELDYFSATPEYISGQINE 24
Db 55 FELPKLPYKXNALEPHISAETLE 77
RESULT 37
US-08-445-909A-17
; Sequence 17, Application US/08445909A
; Patent No. 5772996
; GENERAL INFORMATION:
; APPLICANT: ATKINSON, Antony
; TITLE OF INVENTION: Pharmaceutical Compositions
; TITLE OF INVENTION: Containing Superoxide Dismutase from Bacillus
; TITLE OF INVENTION: Stearotherophilus and Bacillus Caldotenax
; NUMBER OF SEQUENCES: 29
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; TYPE: IBM PC compatible
US-08-445-909A-17
Query Match 36.6%; Score 53; DB 1; Length 204;
Best Local Similarity 37.0%; Pred. No. 0.66;
Matches 10; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
QY 2 YSLPELDYFSATPEYISGQINEIXYT 28
Db 3 FELPALPYDYDALEPHIDKETMNIHT 29
RESULT 38
US-08-445-909A-29
; Sequence 29, Application US/08445909A
; Patent No. 5772996
; GENERAL INFORMATION:
; APPLICANT: ATKINSON, Antony
; TITLE OF INVENTION: Pharmaceutical Compositions
; TITLE OF INVENTION: Containing Superoxide Dismutase from Bacillus
; TITLE OF INVENTION: Stearotherophilus and Bacillus Caldotenax
; NUMBER OF SEQUENCES: 29
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
US-08-445-909A-29
Query Match 36.6%; Score 53; DB 1; Length 204;
Best Local Similarity 37.0%; Pred. No. 0.66;
Matches 10; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
QY 2 YSLPELDYFSATPEYISGQINEIXYT 28
Db 3 FELPALPYDYDALEPHIDKETMNIHT 29
RESULT 39
US-09-252-991A-24593
; Sequence 24593, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,909A
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: US 07/978,697
; APPLICATION NUMBER: US 07/978,697
; FILING DATE: 02-FEB-1993
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-445-909A-17
Query Match 36.6%; Score 53; DB 1; Length 204;
Best Local Similarity 37.0%; Pred. No. 0.66;
Matches 10; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
QY 2 YSLPELDYFSATPEYISGQINEIXYT 28
Db 3 FELPALPYDYDALEPHIDKETMNIHT 29
RESULT 39
US-09-252-991A-24593
; Sequence 24593, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

;/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;/ TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;/ FILE REFERENCE: 107196.1136
;/ CURRENT APPLICATION NUMBER: US/09/252,991A
;/ CURRENT FILING DATE: 1999-02-18
;/ PRIOR APPLICATION NUMBER: US 60/074,788
;/ PRIOR FILING DATE: 1998-02-18
;/ PRIOR APPLICATION NUMBER: US 60/094,190
;/ PRIOR FILING DATE: 1998-07-27
;/ NUMBER OF SEQ ID NOS: 33142
;/ SEQ ID NO 24593
;/ LENGTH: 207
;/ TYPE: PRT
;/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24593

Query Match 35.9%; Score 52; DB 4; Length 207;
Best Local Similarity 37.0%; Pred.No. 0.99;
Matches 10; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 2 YSLPELDYFSAPEYISQINEIXYT 28
Db 7 HALPPPYDAYDALEPHIDALTMEIHHS 33

RESULT 40
US-09-636-215-708
;/ Sequence 708, Application US/09636215
;/ Patent No. 6620922
;/ GENERAL INFORMATION:
;/ APPLICANT: Xu, Jiangchun
;/ APPLICANT: Dillon, Davin C.
;/ APPLICANT: Mitcham, Jennifer L.
;/ APPLICANT: Harlocker, Susan L.
;/ APPLICANT: Jiang, Yuqi
;/ APPLICANT: Henderson, Robert A.
;/ APPLICANT: Kalos, Michael D.
;/ APPLICANT: Fanger, Gary R.
;/ APPLICANT: Retter, Marc W.
;/ APPLICANT: Stolk, John A.
;/ APPLICANT: Day, Craig H.
;/ APPLICANT: Vedvick, Thomas S.
;/ APPLICANT: Carter, Darrick
;/ APPLICANT: Li, Samuel
;/ APPLICANT: Wang, Aijun
;/ APPLICANT: Skeiky, Yasir A. W.
;/ APPLICANT: Hepler, William
;/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
;/ FILE REFERENCE: 210121.42717C17
;/ CURRENT APPLICATION NUMBER: US/09/636,215
;/ CURRENT FILING DATE: 2000-08-10
;/ NUMBER OF SEQ ID NOS: 852
;/ SOFTWARE: FastSeq for Windows Version 3.0
;/ SEQ ID NO 708
;/ LENGTH: 371
;/ TYPE: PRT
;/ ORGANISM: Homo sapiens
US-09-636-215-708

Query Match 34.5%; Score 50; DB 4; Length 371;
Best Local Similarity 45.0%; Pred.No. 4.5;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 YSLPELDYFSAPEYISQ 21
Db 150 YLLPAIDWDTALAPYLGTO 169

Search completed: August 24, 2004, 23:04:24
Job time : 32 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 24, 2004, 23:01:08 ; Search time 124 Seconds
(without alignments)
76.029 Million cell updates/sec

Title: US-09-987-190-2

Perfect score: 145

Sequence: 1 KYSLPELDYEFSAPEYISQINEIXYTX 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1295152 seqs, 314255058 residues

Total number of hits satisfying chosen parameters: 1295152

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	141	97.2	30	9	US-09-987-190-2
2	100	69.0	233	14	US-10-230-331-28
3	79	54.5	30	14	US-10-109-670-52
4	79	54.5	224	14	US-10-109-670-11
5	79	54.5	240	12	US-10-424-599-233245
6	77	53.1	200	9	US-09-818-564-2
7	77	53.1	200	9	US-09-738-626-6727
8	77	53.1	241	12	US-10-230-331-21
9	77	53.1	241	12	US-10-424-599-233247
10	74	51.0	95	9	US-09-993-333-12
11	74	51.0	183	16	US-10-752-791-2
12	74	51.0	222	14	US-10-230-331-19
13	74	51.0	222	14	US-10-230-331-20
14	74	51.0	222	14	US-10-230-331-22
15	74	51.0	222	16	US-10-408-765A-2109

16	72	49.7	228	14	US-10-230-331-25	Sequence 25, Appl
17	71	49.0	188	9	US-09-987-190-6	Sequence 6, Appl
18	70	48.3	214	15	US-10-289-762-75	Sequence 75, Appl
19	70	48.3	233	14	US-10-230-331-24	Sequence 24, Appl
20	68	46.9	213	14	US-10-156-761-12947	Sequence 12947, A
21	67	46.2	198	9	US-09-727-855B-7	Sequence 7, Appl
22	67	46.2	233	15	US-10-310-154-662	Sequence 662, App
23	67	46.2	235	14	US-10-230-331-26	Sequence 26, Appl
24	66	45.5	22	9	US-09-953-510-23	Sequence 23, Appl
25	66	45.5	22	11	US-09-953-413-23	Sequence 23, Appl
26	66	45.5	22	14	US-10-147-255-23	Sequence 23, Appl
27	66	45.5	222	9	US-09-727-855B-5	Sequence 5, Appl
28	65	44.8	80	12	US-10-424-599-184874	Sequence 184874, Appl
29	65	44.8	200	14	US-10-230-331-27	Sequence 27, Appl
30	62	42.8	206	14	US-10-109-670-10	Sequence 10, Appl
31	58	40.0	191	14	US-10-230-331-16	Sequence 16, Appl
32	58	40.0	191	14	US-10-230-331-29	Sequence 29, Appl
33	53	36.6	685	14	US-10-130-973A-7	Sequence 7, Appl
34	53	36.6	862	14	US-10-130-973A-4	Sequence 4, Appl
35	53	36.6	862	14	US-10-130-973A-3	Sequence 3, Appl
36	52.5	36.2	256	12	US-10-425-114-51507	Sequence 51507, A
37	52	35.9	201	15	US-10-310-154-664	Sequence 664, App
38	52	35.9	633	15	US-10-369-493-6225	Sequence 6225, App
39	51.5	35.5	384	16	US-10-437-963-163657	Sequence 163657, Sequence 163658, Sequence 188362, Sequence 5329, App
40	51.5	35.5	770	16	US-10-437-963-163657	Sequence 5329, App
41	51	35.2	171	12	US-10-424-599-188362	Sequence 188362, Sequence 5329, App
42	51	35.2	616	15	US-10-369-493-5329	Sequence 5, Appl
43	50	34.5	326	14	US-10-005-907-5	Sequence 974, App
44	50	34.5	359	9	US-09-822-827-974	Sequence 974, App
45	50	34.5	359	9	US-09-895-793-974	Sequence 974, App

ALIGNMENTS

RESULT 1

US-09-987-190-2
; Sequence 2, Application US/09987190
; Patent No. US20020058293A1
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, Kazutosh
; APPLICANT: MIZUTANI, Shigetoshi
; APPLICANT: ENDO, Masahiro
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: FUNGAL ANTIGENS AND PROCESS FOR PRODUCING THE SAME
; FILE REFERENCE: 1422-0502P
; CURRENT APPLICATION NUMBER: US/09/987,190
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/262,856
; PRIOR FILING DATE: 1999-03-04
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (1)..(30)
; OTHER INFORMATION: any Xaa = any amino acid, unknown or other
US-09-987-190-2

Query Match 97.2%; Score 141; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.6e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSAPEYISQINEIXY 28

DB 1 KYSLPELDYEFSAPEYISQINEIXY 28

RESULT 2

US-10-230-331-28

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; Sequence 28, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-230-331-28

Query Match 69.0%; Score 100; DB 14; Length 233;
Best Local Similarity 64.3%; Pred. No. 8.1e-07;
Matches 18; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 KYSLPELDYFSGATEPYISQINEIXY 28
Db 27 KYTLPDLKWDGFALEPAISGEIMELHYT 54

RESULT 3
US-10-109-670-52
; Sequence 52, Application US/10109670
; Publication No. US20030105283A1
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH et al.
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA
; FILE REFERENCE: 1422-0523P
; CURRENT APPLICATION NUMBER: US/10/109,670
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 52
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Malassezia furfur
US-10-109-670-52

Query Match 54.5%; Score 79; DB 14; Length 30;
Best Local Similarity 55.6%; Pred. No. 0.00012;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 KYSLPELDYFSGATEPYISQINEIXY 27
Db 1 KYTLPPLPYDYGALEPAISGEIMETHY 27

RESULT 4
US-10-109-670-11
; Sequence 11, Application US/10109670
; Publication No. US20030105283A1
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH et al.
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA
; FILE REFERENCE: 1422-0523P
; CURRENT APPLICATION NUMBER: US/10/109,670
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 11
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Malassezia furfur
US-10-109-670-11

Query Match 54.5%; Score 79; DB 14; Length 224;
Best Local Similarity 55.6%; Pred. No. 0.0011;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

; Sequence 28, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-230-331-28

Query Match 69.0%; Score 100; DB 14; Length 233;
Best Local Similarity 64.3%; Pred. No. 8.1e-07;
Matches 18; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 KYSLPELDYFSGATEPYISQINEIXY 28
Db 27 KYTLPDLKWDGFALEPAISGEIMELHYT 54

RESULT 3
US-10-109-670-52
; Sequence 52, Application US/10109670
; Publication No. US20030105283A1
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH et al.
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA
; FILE REFERENCE: 1422-0523P
; CURRENT APPLICATION NUMBER: US/10/109,670
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 52
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Malassezia furfur
US-10-109-670-52

Query Match 54.5%; Score 79; DB 14; Length 30;
Best Local Similarity 55.6%; Pred. No. 0.00012;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 KYSLPELDYFSGATEPYISQINEIXY 27
Db 1 KYTLPPLPYDYGALEPAISGEIMETHY 27

RESULT 4
US-10-109-670-11
; Sequence 11, Application US/10109670
; Publication No. US20030105283A1
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH et al.
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA
; FILE REFERENCE: 1422-0523P
; CURRENT APPLICATION NUMBER: US/10/109,670
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 11
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Malassezia furfur
US-10-109-670-11

Query Match 54.5%; Score 79; DB 14; Length 224;
Best Local Similarity 55.6%; Pred. No. 0.0011;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

; Sequence 28, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-230-331-28

Query Match 69.0%; Score 100; DB 14; Length 233;
Best Local Similarity 64.3%; Pred. No. 8.1e-07;
Matches 18; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 KYSLPELDYFSGATEPYISQINEIXY 27
Db 25 KYTLPPLPYDYGALEPAISGEIMETHY 51

RESULT 5
US-10-424-599-233245
; Sequence 233245, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 233245
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_52646C.1.pep
US-10-424-599-233245

Query Match 54.5%; Score 79; DB 12; Length 240;
Best Local Similarity 50.0%; Pred. No. 0.0012;
Matches 13; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 2 YSLPELDYFSGATEPYISQINEIXY 27
Db 40 YTLPLDLDYGALEPAISGEIMQLHH 65

RESULT 6
US-09-818-564-2
; Sequence 2, Application US/09818564
; Patent No. US20020137151A1
; GENERAL INFORMATION:
; APPLICANT: MERKAM, MURIEL
; APPLICANT: GUYONVARCH, ARMEL
; APPLICANT: MARX, ACHIM
; TITLE OF INVENTION: A PROCESS FOR THE FERMENTATIVE PREPARATION OF METABOLIC
; TITLE OF INVENTION: PRODUCTS AND FOR THE NUCLEOTIDE SEQUENCES ENCODING FOR
; TITLE OF INVENTION: THE SOD GENE
; FILE REFERENCE: 21123/278411/MAS
; CURRENT APPLICATION NUMBER: US/09/818,564
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 09/373,731
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Corynebacterium melassecola
; OTHER INFORMATION: ATCC 17965
US-09-818-564-2

Query Match 53.1%; Score 77; DB 9; Length 200;
Best Local Similarity 48.1%; Pred. No. 0.0019;
Matches 13; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 YSLPELDYFSGATEPYISQINEIXY 28
Db 4 YELPELDYADALEPHIAAEIMELHHS 30

RESULT 7
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US-10-424-599-233247
; Sequence 233247, Application US/10424599

; CURRENT FILING DATE: 2004-01-07
 : PRIOR APPLICATION NUMBER: US/08/003 025C

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RESULT 11
US-10-752-791-2
; Sequence 2, Application US/10752791
; Publication No. US20040152115A1
; GENERAL INFORMATION:
; APPLICANT: Anziano, Paul Q.
; TITLE OF INVENTION: Manganese Superoxide Dismutase Exon 3-Deleted Isoforms
; TITLE OF INVENTION: and Nucleic Acid Molecules Encoding the Isoforms
; FILE REFERENCE: 53073-0001-US
; CURRENT APPLICATION NUMBER: US/10/752,791
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US/09/623,025C

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; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/075,948
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: PCT/US99/04129
; PRIOR FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-752-791-2

Query Match      51.0%; Score 74; DB 16; Length 183;
Best Local Similarity 42.9%; Pred. No. 0.005;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDYEFSAPEYISQINEIXYT 28
   |||||::: |||||::: |||||:::
Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 12
US-10-230-331-19
; Sequence 19, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-331-19

Query Match      51.0%; Score 74; DB 14; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0062;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDYEFSAPEYISQINEIXYT 28
   |||||::: |||||::: |||||:::
Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 13
US-10-230-331-20
; Sequence 20, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-230-331-20

Query Match      51.0%; Score 74; DB 14; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0062;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDYEFSAPEYISQINEIXYT 28
   |||||::: |||||::: |||||:::
Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 14
US-10-230-331-22
; Sequence 22, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-230-331-22

Query Match      51.0%; Score 74; DB 14; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0062;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDYEFSAPEYISQINEIXYT 28
   |||||::: |||||::: |||||:::
Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 15
US-10-408-765A-2109
; Sequence 2109, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2109
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2109

Query Match      51.0%; Score 74; DB 16; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0062;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDYEFSAPEYISQINEIXYT 28
   |||||::: |||||::: |||||:::
Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 16
US-10-230-331-25
; Sequence 25, Application US/10230331

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Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDYEFSAPEYISQINEIXYT 28
   |||||::: |||||::: |||||:::
Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 14
US-10-230-331-22
; Sequence 22, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-230-331-22

Query Match      51.0%; Score 74; DB 14; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0062;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDYEFSAPEYISQINEIXYT 28
   |||||::: |||||::: |||||:::
Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 15
US-10-408-765A-2109
; Sequence 2109, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2109
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2109

Query Match      51.0%; Score 74; DB 16; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0062;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDYEFSAPEYISQINEIXYT 28
   |||||::: |||||::: |||||:::
Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 16
US-10-230-331-25
; Sequence 25, Application US/10230331

```

```
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Capsicum annuum
US-10-230-331-25

Query Match      49.7%; Score 72; DB 14; Length 228;
Best Local Similarity 46.2%; Pred. No. 0.013;
Matches 12; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY      2 YSLPELDYFSAPEYISQINEIXY 27
Db      28 FSLPDLSDYDGALEPAISGEIMQLHH 53

RESULT 17
US-09-987-190-6
; Sequence 6, Application US/09987190
; Patent No. US20020058293A1
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, Kazutoh
; APPLICANT: MIZUTANI, Shigetoshi
; APPLICANT: ENDO, Masahiro
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: FUNGAL ANTIGENS AND PROCESS FOR PRODUCING THE SAME
; FILE REFERENCE: 1422-0502P
; CURRENT APPLICATION NUMBER: US/09/987,190
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/262,856
; PRIOR FILING DATE: 1999-03-04
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-987-190-6

Query Match      49.0%; Score 71; DB 9; Length 188;
Best Local Similarity 81.2%; Pred. No. 0.014;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      13 ATEPYISQINEIXYT 28
Db      1 ATEPYITQONEIHYT 16

RESULT 18
US-10-289-762-75
; Sequence 75, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 75
; LENGTH: 214
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; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-75

Query Match      48.3%; Score 70; DB 15; Length 214;
Best Local Similarity 61.9%; Pred. No. 0.024;
Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      2 YSLPELDYFSAPEYISQI 22
Db      13 YSLPELDYDGALEPVISSEI 33

RESULT 19
US-10-230-331-24
; Sequence 24, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTE
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Pisum sativum
US-10-230-331-24

Query Match      48.3%; Score 70; DB 14; Length 233;
Best Local Similarity 46.2%; Pred. No. 0.026;
Matches 12; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY      2 YSLPELDYFSAPEYISQINEIXY 27
Db      40 FTLPDLAYDGALEPVISGEIMQIHH 65

RESULT 20
US-10-156-761-12947
; Sequence 12947, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 12947
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12947

Query Match      46.9%; Score 68; DB 14; Length 213;
Best Local Similarity 50.0%; Pred. No. 0.047;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
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```
Qy 2 YSLPELDYEFSAPEYISQGINEIXY 27
Db 4 YTLPELDYDYSALAPVISPEIHLHH 29

RESULT 21
US-09-727-855B-7
; Sequence 7, Application US/09727855B
; Patent No. US20020168703A1
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OIUMA, Kazuyuki
; TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFUL
; TITLE OF INVENTION: MATERIALS THEREOF
; FILE REFERENCE: C38435/111694
; CURRENT APPLICATION NUMBER: US/09/727,855B
; CURRENT FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Phaffia rhodozyma
US-09-727-855B-7

Query Match 46.2%; Score 67; DB 9; Length 198;
Best Local Similarity 57.1%; Pred. No. 0.061;
Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 2 YSLPELDYEFSAPEYISQGINEIXY 22
Db 4 YTLPELDYDYSALAPVISPEIHLHH 24

RESULT 22
US-10-310-154-662
; Sequence 662, Application US/10310154
; Publication No. US20030233670A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Chomet, Paul S.
; APPLICANT: Adams, Thomas H
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Agarwal, Ameeta K.
; APPLICANT: Ahrens, Jeffrey E.
; APPLICANT: Ball, James A.
; APPLICANT: Banu, G.
; APPLICANT: Bell, Erin
; APPLICANT: Boddupalli, Raghava
; APPLICANT: Deikman, Jill
; APPLICANT: Deng, Molian
; APPLICANT: Dong, Jinzhao
; APPLICANT: Duff, Stephen M.
; APPLICANT: Galligan, Meghan M.
; APPLICANT: Hinchey, Brenda S.
; APPLICANT: Huang, Shihshieh
; APPLICANT: Johnson, G. Richard
; APPLICANT: Jung, Vincent
; APPLICANT: Kretzmer, Keith A.
; APPLICANT: Laccetti, Lucille B.
; APPLICANT: Lai, Chao-Qiang
; APPLICANT: Lee, Gary
; APPLICANT: Lin, Jie-Yi
; APPLICANT: Liu, Jingdong
; APPLICANT: Lu, Bin
; APPLICANT: Luethy, Michael M.
; APPLICANT: Lund, Adrian
; APPLICANT: Madson, Linda L.
; APPLICANT: Malloy, Kathleen A.
; APPLICANT: McKiel, Christine L.
; APPLICANT: Miller, Philip W.
; APPLICANT: Padmavathi, Manchikanti

Query Match 46.2%; Score 67; DB 9; Length 198;
Best Local Similarity 57.1%; Pred. No. 0.061;
Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 2 YSLPELDYEFSAPEYISQGINEIXY 27
Db 4 YTLPELDYDYSALAPVISPEIHLHH 29

RESULT 23
US-10-230-331-26
; Sequence 26, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTE.
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 26
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Zea mays
US-10-230-331-26

Query Match 46.2%; Score 67; DB 14; Length 235;
Best Local Similarity 48.0%; Pred. No. 0.074;
Matches 12; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 3 SLPELDYEFSAPEYISQGINEIXY 27
Db 36 TLPDLSDYDFGALEPAISGEIMRLHH 60

RESULT 24
US-09-953-510-23
; Sequence 23, Application US/09953510
; Patent No. US20020131975A1
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Marcus A.
; TITLE OF INVENTION: Abundant Extracellular
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
```

```
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Start, William G.
; APPLICANT: Tennesen, Dan
; APPLICANT: Vidya, K.R.
; APPLICANT: Wang, Haiyuo
; APPLICANT: Xin, Zhanqun
; APPLICANT: Xu, Nanfei
; APPLICANT: Yang, Chunzhi
; APPLICANT: Zeng, Xiaoping
; APPLICANT: Zhang, Qiang
; APPLICANT: Zhao, Yajuan
; APPLICANT: Zhou, Li
; TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
; FILE REFERENCE: 38-15(52796)B
; CURRENT APPLICATION NUMBER: US/10/310,154
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,358
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 736
; SEQ ID NO 662
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Zea mays
US-10-310-154-662

Query Match 46.2%; Score 67; DB 15; Length 233;
Best Local Similarity 48.0%; Pred. No. 0.074;
Matches 12; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 3 SLPELDYEFSAPEYISQGINEIXY 27
Db 34 ALPDLSDYDFGALEPAISGEIMRLHH 58

RESULT 25
US-10-230-331-26
; Sequence 26, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTE.
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 26
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Zea mays
US-10-230-331-26

Query Match 46.2%; Score 67; DB 14; Length 235;
Best Local Similarity 48.0%; Pred. No. 0.074;
Matches 12; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 3 SLPELDYEFSAPEYISQGINEIXY 27
Db 36 TLPDLSDYDFGALEPAISGEIMRLHH 60

RESULT 26
US-09-953-510-23
; Sequence 23, Application US/09953510
; Patent No. US20020131975A1
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Marcus A.
; TITLE OF INVENTION: Abundant Extracellular
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
```



```

; ADDRESSEE: Kurt A. MacLean
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/953,510
; FILING DATE: 14-Sep-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/447,398
; FILING DATE: 23-MAY-1995
; APPLICATION NUMBER: US 08/289,667
; FILING DATE: 12-AUG-1994
; APPLICATION NUMBER: US 08/156,358
; FILING DATE: 23-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLean, Kurt A.
; REGISTRATION NUMBER: 31,118
; REFERENCE/DOCKET NUMBER: 112-272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 777-1297
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; STRAIN: Erdman
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
;
; US-09-953-510-23
;
; Query Match 45.5%; Score 66; DB 9; Length 22;
; Best Local Similarity 61.1%; Pred. No. 0.0073;
; Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
;
; QY 4 LPELDVEFSATEPYISGQ 21
; Db 5 LPDLWDYGALEPHISGQ 22
;
; RESULT 25
; US-09-953-413-23
; Sequence 23, Application US/09953413
; Publication No. US20040018209A1
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Marcus A.
; TITLE OF INVENTION: Abundant Extracellular
; Products and Methods for Their Production and Use
;
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kurt A. MacLean
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/147,255
; FILING DATE: 15-May-2002
; CLASSIFICATION: <Unknown>

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/953,413
; FILING DATE: 14-Sep-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/447,398
; FILING DATE: 23-MAY-1995
; APPLICATION NUMBER: US 08/289,667
; FILING DATE: 12-AUG-1994
; APPLICATION NUMBER: US 08/156,358
; FILING DATE: 23-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLean, Kurt A.
; REGISTRATION NUMBER: 31,118
; REFERENCE/DOCKET NUMBER: 112-272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 777-1297
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; STRAIN: Erdman
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
;
; US-09-953-413-23
;
; Query Match 45.5%; Score 66; DB 11; Length 22;
; Best Local Similarity 61.1%; Pred. No. 0.0073;
; Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
;
; QY 4 LPELDVEFSATEPYISGQ 21
; Db 5 LPDLWDYGALEPHISGQ 22
;
; RESULT 26
; US-10-147-255-23
; Sequence 23, Application US/10147255
; Publication No. US20030152584A1
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Marcus A.
; TITLE OF INVENTION: Abundant Extracellular
; Products and Methods for Their Production and Use
;
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kurt A. MacLean
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/147,255
; FILING DATE: 15-May-2002
; CLASSIFICATION: <Unknown>

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/226,539A
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/447,398
; FILING DATE: 23-MAY-1995
; APPLICATION NUMBER: US 08/289,667
; FILING DATE: 12-AUG-1994
; APPLICATION NUMBER: US 08/156,358
; FILING DATE: 23-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLean, Kurt A.
; REGISTRATION NUMBER: 31,118
; REFERENCE/DOCKET NUMBER: 112-272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 277-1297
; INFORMATION FOR SEQ ID NO: 23:
; STRAIN: Erdman
; ORGANISM: Mycobacterium tuberculosis
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-147-255-23

Query Match 45.5%; Score 66; DB 14; Length 22;
Best Local Similarity 61.1%; Pred. No. 0.0073;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 4 LPDLDFYSATEPYISQ 21
Db 5 LPDLWDYGALEPHISQ 22

RESULT 27
US-09-727-855B-5
; Sequence 5, Application US/09727855B
; Patent No. US20020168703A1
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOCIDS AND BIOLOGICALLY USEFUL
; FILE REFERENCE: C38435/111694
; CURRENT APPLICATION NUMBER: US/09/727,855B
; CURRENT FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Phaffia rhodozyma
US-09-727-855B-5

Query Match 45.5%; Score 66; DB 9; Length 222;
Best Local Similarity 46.4%; Pred. No. 0.098;
Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 KYSLPDLDFYSATEPYISQINEIXT 28
Db 26 KHTLPDPYDALEPSISKELWILHHT 53

RESULT 28
US-10-424-599-184874
```

```
; Sequence 184874, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(S3223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 184874
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(80)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_137957C.1.pap
US-10-424-599-184874

Query Match 44.8%; Score 65; DB 12; Length 80;
Best Local Similarity 42.3%; Pred. No. 0.044;
Matches 11; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 2 YSLPDLDFYSATEPYISQINEIXY 27
Db 32 YTLPLDLDYDXALEPAXSXDMQLHH 57

RESULT 29
US-10-230-331-27
; Sequence 27, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTE.
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Ganoderma microsporum
US-10-230-331-27

Query Match 44.8%; Score 65; DB 14; Length 200;
Best Local Similarity 50.0%; Pred. No. 0.12;
Matches 12; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 4 LPDLDFYSATEPYISQINEIXY 27
Db 5 LPDLPAYNALEPFISQIMELHH 28

RESULT 30
US-10-109-670-10
; Sequence 10, Application US/10109670
; Publication No. US20030105283A1
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH et al.
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA
; FILE REFERENCE: 1422-0523P
; CURRENT APPLICATION NUMBER: US/10/109,670
; CURRENT FILING DATE: 2002-04-01
```

```
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 10
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Malassezia furfur
US-10-109-670-10

Query Match      42.8%; Score 62; DB 14; Length 206;
Best Local Similarity 40.7%; Pred. No. 0.36;
Matches 11; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 KYSLPDYEFSAPEYISGQINEIXYT 27
    :||| : : ||| : :
Db 6 EYTLPLPYADALEPFIKSEIMTVHH 32
    :||| : : ||| : :

RESULT 31
US-10-230-331-16
; Sequence 16, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Superoxide Dismutase Protein Sequence
US-10-230-331-16

Query Match      40.0%; Score 58; DB 14; Length 191;
Best Local Similarity 44.0%; Pred. No. 1.3;
Matches 11; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 4 LPELDYEFSATEPYISGQINEIXYT 28
    ||| : : ||| ||| : :
Db 11 LPKLPPAYNALEPAISSQIMELHHS 35
    ||| : : ||| ||| : :

RESULT 32
US-10-230-331-29
; Sequence 29, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Rhodotorula glutinis
US-10-230-331-29

Query Match      40.0%; Score 58; DB 14; Length 191;
Best Local Similarity 44.0%; Pred. No. 1.3;
Matches 11; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 4 LPELDYEFSATEPYISGQINEIXYT 28
    ||| : : ||| ||| : :
Db 11 LPKLPPAYNALEPAISSQIMELHHS 35
    ||| : : ||| ||| : :

RESULT 33
US-10-130-973A-7
; Sequence 7, Application US/10130973A
; Publication No. US20030147895A1
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford
; APPLICANT: Sutton, John
; APPLICANT: Silman, Nigel
; TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
; FILE REFERENCE: 1581.0920000
; CURRENT APPLICATION NUMBER: US/10/130,973A
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: PCT/GB00/04644
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: GB 9928530.6
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: GB 008658.7
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-130-973A-7

Query Match      36.6%; Score 53; DB 14; Length 685;
Best Local Similarity 37.0%; Pred. No. 31;
Matches 10; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy 2 YSLPELDYEFSAPEYISGQINEIXYT 28
    :||| : : ||| : :
Db 3 FELPALPYDALEPHIDKRTWNIHT 29
    :||| : : ||| : :

RESULT 34
US-10-130-973A-4
; Sequence 4, Application US/10130973A
; Publication No. US20030147895A1
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford
; APPLICANT: Sutton, John
; APPLICANT: Silman, Nigel
; TITLE OF INVENTION: Constructs for Delivery of Therapeutic Agents to Neuronal Cells
; FILE REFERENCE: 1581.0920000
; CURRENT APPLICATION NUMBER: US/10/130,973A
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: PCT/GB00/04644
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: GB 9928530.6
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: GB 008658.7
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 862
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-130-973A-4

Query Match      36.6%; Score 53; DB 14; Length 862;
Best Local Similarity 37.0%; Pred. No. 41;
Matches 10; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy 2 YSLPELDYEFSAPEYISGQINEIXYT 28
    :||| : : ||| : :
Db 3 FELPALPYDALEPHIDKRTWNIHT 29
    :||| : : ||| : :
```

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Query Match      36.2%; Score 52.5; DB 12; Length 256;
Best Local Similarity 52.4%; Pred. NO. 12;
Matches 11; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

Qy      1 KYSLPGLDYFSAPEYISQ 21
      ::|||::|::|::|::|
pb      201 EFPNFIAYKFSVTDP-ISG 220

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RESULT 40

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 24, 2004, 22:48:16 ; Search time 23 Seconds
(without alignments)
67.918 Million cell updates/sec

Title: US-09-987-190-2

Perfect score: 145

Sequence: 1 KYSLPELYRFSATEPYISQINEIXYTX 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	141	97.2	234	1	SODM_CANAL
2	103	71.0	206	1	SODM_NOCAS
3	101	69.7	206	1	SODM_MYCAV
4	100	69.0	206	1	SODM_MYCLP
5	100	69.0	233	1	SODM_YEAST
6	99	68.3	206	1	SODM_MYCFO
7	98	68.3	206	1	SODM_MYCSM
8	98	67.6	206	1	SODM_MYCLE
9	94	64.8	207	1	SODF_MYCTU
10	91	62.8	201	1	SODM_PROFR
11	83	57.2	245	1	SODM_NEUCR
12	80	55.2	222	1	SODM_HORSE
13	78	53.8	199	1	SODM_CORDI
14	77	53.1	202	1	SODM_RABIT
15	76	52.4	202	1	SODF_METJ
16	74	51.0	198	1	SODM_CALJA
17	74	51.0	198	1	SODM_CEBAP
18	74	51.0	198	1	SODM_HYLLA
19	74	51.0	198	1	SODM_MACFA
20	74	51.0	198	1	SODM_MACFA
21	74	51.0	198	1	SODM_MACMU
22	74	51.0	198	1	SODM_PANTR
23	74	51.0	198	1	SODM_PONPY
24	74	51.0	211	1	SODF_ACIAM
25	74	51.0	222	1	SODM_BOVIN
26	74	51.0	222	1	SODM_HUMAN
27	74	51.0	222	1	SODM_MOUSE
28	74	51.0	222	1	SODM_RAT
29	73	50.3	210	1	SODF_SULSO
30	72	49.7	211	1	SODF_PRAE
31	72	49.7	228	1	SODM_CAPAN
32	71	49.0	210	1	SODM_ASFFU
33	71	49.0	233	1	SODM_HEVBR

34 70 48.3 203 1 SODM_BORBU
35 70 48.3 207 1 SODM_CHLPN
36 70 48.3 231 1 SODM_ARATH
37 70 48.3 233 1 SODM_PEA
38 70 48.3 281 1 SODF_BAGSU
39 69 47.6 228 1 SODM_NICPL
40 68 46.9 200 1 SODM_AGABI
41 68 46.9 210 1 SODF_SULAC
42 68 46.9 211 1 SODM_CAVPO
43 68 46.9 212 1 SODF_STRCO
44 68 46.9 232 1 SODN_MAIZE
45 68 46.9 233 1 SODO_MAIZE

ALIGNMENTS

RESULT 1
ID SODM_CANAL STANDARD; PRT; 234 AA.
AC O13401;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
GN SOD2
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
RX MEDLINE=99177433; PubMed=10076057;
RA Rhie G.E., Hwang C.S., Brady M.J., Kim S.T., Kim Y.R., Huh W.K.,
BAEK Y.U., Lee B.H., Lee J.S., Kang S.O.;
RT "Manganese-containing superoxide dismutase and its gene from Candida albicans";
RL Biochim. Biophys. Acta 1426:409-419(1999).
CC -!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase family.

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EMBL: AF031478; AAB86583.1; --
HSSP: P04179; IABW.
DR InterPro: IPR001189; SODismutase.
DR Pfam: PF00081; sodfe; 1.
DR Pfam: PF02777; sodfe_C; 1.
DR PRINTS: PR01703; MNSODISMWTASE.
DR ProDom: PD000475; SODISMUTASE; 1.
DR PROSITE: PS00088; SOD_MN; 1.
KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
KW Transit peptide.
FT TRANSIT 1 34 MITOCHONDRION.
FT CHAIN 35 234 SUPEROXIDE DISMUTASE [MN].
FT METAL 60 60 MANGANESE (BY SIMILARITY).
FT METAL 108 108 MANGANESE (BY SIMILARITY).
FT METAL 198 198 MANGANESE (BY SIMILARITY).
FT METAL 202 202 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 234 AA; 26173 MW; EBFEC2D769C1D9C1 CRC64;

Search 9


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RC STRAIN=Hawaiian;
RA Nakamura M.;
RL Submitted (SEP-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC -----
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CC -----
DR EMBL; D13288; BAA28850.1; -.
DR HSSP; P17670; IIDS.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF000081; sodfe_1.
DR Pfam; PF02777; sodfe_C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
DR Oxidoreductase; Metal-binding; Manganese.
DR INIT_MET 0 BY SIMILARITY.
FT METAL 27 27 MANGANESE (BY SIMILARITY).
FT METAL 75 75 MANGANESE (BY SIMILARITY).
FT METAL 159 159 MANGANESE (BY SIMILARITY).
FT METAL 163 163 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 206 AA; 23031 MW; 92A063471FA9F22F CRC64;

Query Match 69.0%; Score 100; DB 1; Length 206;
Best Local Similarity 60.7%; Pred. No. 1.3e-07;
Matches 17; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSSATEPYISGQINEIXYT 28
Db 2 EYLPDLWDYEALEPHISGQINEIHT 29

RESULT 5
SODM YEAST
ID SODM YEAST STANDARD; PRT; 233 AA.
AC P00447;
DT 21-JUL-1986 (Rel. 01, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
GN SOD2 OR YHR008C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85127011; PubMed=3882422;
RA Marrs C.A.M., van Loon A.P.G.M., Oudshoorn P., van Steeg H.,
RA Grivell L.A., Slater E.C.;
RA "Nucleotide sequence analysis of the nuclear gene coding for
RT manganese superoxide dismutase of yeast mitochondria, a gene
RT previously assumed to code for the Rieske iron-sulphur protein.";
RL Eur. J. Biochem. 147:153-161(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
RA Kucaba T., Hillier L.W., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,

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RA Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
RA Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VIII.";
RL Science 265:2077-2082(1994).
RN [3]
RP SEQUENCE OF 1-39 FROM N.A.
RX MEDLINE=89211942; PubMed=3072251;
RA Schrank I.S., Sims P.F., Oliver S.G.;
RT "Functional expression of the yeast Mn-superoxide dismutase gene in
RT Escherichia coli requires deletion of the signal peptide sequence.";
RL Gene 73:121-130(1988).
RN [4]
RP SEQUENCE OF 27-233.
RA Ditlow C., Johansen J.T., Martin B.M., Svendsen I.;
RT "The complete amino acid sequence of manganese-superoxide dismutase
RT from Saccharomyces cerevisiae.";
RL Carlsberg Res. Commun. 47:81-91(1982).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC -----
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CC -----
DR EMBL; X02156; CAA26092.1; -.
DR EMBL; U10400; AAB88939.1; -.
DR EMBL; M24079; AAA35065.1; -.
DR PIR; A00521; DSBYN.
DR HSSP; P04179; IABM.
DR GermOnline; 139325; -.
DR SGD; S0001050; SOD2.
DR GO; GO:0005759; C:mitochondrial matrix; IDA.
DR GO; GO:0008383; F:manganese superoxide dismutase activity; IDA.
DR GO; GO:0006800; P:oxygen and reactive oxygen species metabolism; IMP.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe_1.
DR Pfam; PF02777; sodfe_C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
DR Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
KW Transit peptide.
FT TRANSIT 1 26 MITOCHONDRION
FT CHAIN 27 233 SUPEROXIDE DISMUTASE [MN].
FT METAL 52 52 MANGANESE (BY SIMILARITY).
FT METAL 107 107 MANGANESE (BY SIMILARITY).
FT METAL 194 194 MANGANESE (BY SIMILARITY).
FT METAL 198 198 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 233 AA; 25774 MW; 88A9391FBB31D06E CRC64;

Query Match 69.0%; Score 100; DB 1; Length 233;
Best Local Similarity 64.3%; Pred. No. 1.4e-07;
Matches 18; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSSATEPYISGQINEIXYT 28
Db 27 KVTLPDLKWDGFALEFYISGQINEIHYT 54

RESULT 6
SODM_MYCFO

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ID SODM_MYCFO STANDARD; PRT; 206 AA.
AC Q59519;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn] (EC 1.15.1.1).
GN SODA OR SOD.
OS Mycobacterium fortuitum.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1766;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=1-2C;
RX MEDLINE=99134360; PubMed=9933629;
RA Harth G., Horwitz M.A.;
RT "Export of recombinant Mycobacterium tuberculosis superoxide dismutase
is dependent upon both information in the protein and mycobacterial
export machinery. A model for studying the export of leaderless proteins
by pathogenic mycobacteria.";
RL J. Biol. Chem. 274:4281-4292(1999).
RN [2]
RP REVISIONS TO 116 AND 201.
RA Tullius M.V., Harth G., Horwitz M.A.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 27-164 FROM N.A.
RC STRAIN=NCTC 10265 / ATCC 14468 / W-113;
RX Bull T.J., Shanson D.C., Archard L.C.;
RA "Rapid identification of mycobacteria from AIDS patients by capillary
RT electrophoretic profiling of amplified SOD gene.";
RL J. Clin. Pathol. Clin. Mol. Pathol. 48:124-132(1995).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC
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CC
CC EMBL; X70914; CAA50266.1; -.
CC PIR; S60669; S60669.
CC HSP; P17670; 1IDS.
CC InterPro; IPR001189; SODismutase.
CC Pfam; PF00081; sodfe; 1.
CC PRINTS; PR01703; MNSODISMUTASE.
CC ProDom; PD000475; SODismutase; 1.
CC PROSITE; PS00088; SOD_MN; 1.
CC Oxidoreductase; Metal-binding; Manganese.
CC INIT_MET 0
CC BY SIMILARITY.
CC METAL 27 27 MANGANESE (BY SIMILARITY).
CC FT METAL 75 75 MANGANESE (BY SIMILARITY).
CC FT METAL 159 159 MANGANESE (BY SIMILARITY).
CC FT METAL 163 163 MANGANESE (BY SIMILARITY).
CC SEQUENCE 206 AA; 22833 MW; 500625A8B9321246 CRC64;
Query Match 68.3%; Score 99; DB 1; Length 206;
Best Local Similarity 57.1%; Pred. No. 1.8e-07;
Matches 16; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
Qy 1 KYSLPELDYEFSAPEYISQINELXYT 28
Db 2 EYTLPLDLDYDYGALPHISQINELHHS 29
RESULT 7
SODM_MYCSM STANDARD; PRT; 206 AA.
AC P53649; Q9S612;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn] (EC 1.15.1.1).
GN SODA OR SOD.
OS Mycobacterium smegmatis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1772;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=1-2C;
RX MEDLINE=99134360; PubMed=9933629;
RA Harth G., Horwitz M.A.;
RT "Export of recombinant Mycobacterium tuberculosis superoxide dismutase
is dependent upon both information in the protein and mycobacterial
export machinery. A model for studying the export of leaderless proteins
by pathogenic mycobacteria.";
RL J. Biol. Chem. 274:4281-4292(1999).
RN [2]
RP REVISIONS TO 116 AND 201.
RA Tullius M.V., Harth G., Horwitz M.A.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 27-164 FROM N.A.
RC STRAIN=NCTC 10265 / ATCC 14468 / W-113;
RX Bull T.J., Shanson D.C., Archard L.C.;
RA "Rapid identification of mycobacteria from AIDS patients by capillary
RT electrophoretic profiling of amplified SOD gene.";
RL J. Clin. Pathol. Clin. Mol. Pathol. 48:124-132(1995).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC
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CC
CC EMBL; AF061031; AAD15825.2; -.
CC PIR; S52366; S52366.
CC HSP; P17670; 1IDS.
CC InterPro; IPR001189; SODismutase.
CC Pfam; PF00081; sodfe; 1.
CC PRINTS; PR01703; MNSODISMUTASE.
CC ProDom; PD000475; SODismutase; 1.
CC PROSITE; PS00088; SOD_MN; 1.
CC Oxidoreductase; Metal-binding; Manganese.
CC INIT_MET 0
CC BY SIMILARITY.
CC METAL 27 27 MANGANESE (BY SIMILARITY).
CC FT METAL 75 75 MANGANESE (BY SIMILARITY).
CC FT METAL 159 159 MANGANESE (BY SIMILARITY).
CC FT METAL 163 163 MANGANESE (BY SIMILARITY).
CC SEQUENCE 206 AA; 22804 MW; B997A1AD0374AEC9 CRC64;
Query Match 68.3%; Score 99; DB 1; Length 206;
Best Local Similarity 57.1%; Pred. No. 1.8e-07;
Matches 16; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
Qy 1 KYSLPELDYEFSAPEYISQINELXYT 28
Db 2 EYTLPLDLDYDYGALPHISQINELHHS 29
RESULT 8
SODM_MYCLE STANDARD; PRT; 206 AA.
AC P13367;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn] (EC 1.15.1.1).

```


Submitted (SEP-1997) to the PDB data bank.
 [4] X-RAY CRYSTALLOGRAPHY (1.35 ANGSTROMS).
 MEDLINE=99248073; PubMed=10231372;
 Schmidt M.;
 "Manipulating the coordination number of the ferric iron within the
 cambialistic superoxide dismutase of *Propionibacterium shermanii* by
 changing the pH-value. A crystallographic analysis.";
 Eur. J. Biochem. 262:117-127(1999).
 -!- FUNCTION: Destroys radicals which are normally produced within the
 cells and which are toxic to biological systems.
 -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 -!- COFACTOR: Binds 1 manganese or iron ion per subunit.
 -!- SUBUNIT: Homotetramer.
 -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
 family.
 PIR; JC4396.
 DR PDB; 1AR4; 12-NOV-97.
 DR PDB; 1AR5; 12-NOV-97.
 DR PDB; 1AVM; 18-MAR-98.
 DR PDB; 1BS3; 15-JUN-99.
 DR PDB; 1BSN; 15-JUN-99.
 DR PDB; 1BT8; 15-JUN-99.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF000081; sodfe; 1.
 DR Pfam; PF02777; sodfe; 1.
 DR PRINTS; PR01703; MNSODISMUTASE.
 DR PRODOM; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD_MN; 1.
 DR Oxidoreductase; Metal-binding; Manganese; Iron; 3D-structure.
 KW METAL 27 27 MANGANESE OR IRON.
 FT METAL 75 75 MANGANESE OR IRON.
 FT METAL 161 161 MANGANESE OR IRON.
 FT METAL 165 165 MANGANESE OR IRON.
 FT TURN 12 18
 FT HELIX 21 29
 FT TURN 30 30
 FT HELIX 31 52
 FT TURN 53 53
 FT TURN 55 57
 FT TURN 58 80
 FT TURN 81 81
 FT STRAND 82 82
 FT TURN 85 86
 FT HELIX 94 104
 FT HELIX 107 119
 FT TURN 120 120
 FT STRAND 125 132
 FT TURN 133 136
 FT STRAND 137 144
 FT TURN 145 147
 FT STRAND 148 148
 FT TURN 152 153
 FT STRAND 155 161
 FT HELIX 164 166
 FT TURN 167 167
 FT TURN 171 168
 FT TURN 172 173
 FT TURN 175 182
 FT HELIX 183 185
 FT STRAND 186 186
 FT HELIX 188 198
 FT TURN 199 199
 SQ SEQUENCE 201 AA; 22633 MW; 5BFF424C7B32E00 CRC64;
 Query Match 62.8%; Score 91; DB 1; Length 201;
 Best Local Similarity 61.5%; Pred. No. 2.7e-06;
 Matches 16; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 QY 2 YSLPELDVEFSATEPYISQINEIXY 27
 DB 3 YTLPELDYDYSALEPYISQINEIMELH 28

RESULT 11
 SODM_NEUCR
 ID SODM_NEUCR STANDARD; PRT; 245 AA.
 AC Q9Y783;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Superoxide dismutase [Mn], mitochondrial precursor (RC 1.15.1.1).
 GN SOD-2 OR 18F11.030.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 SEQUENCE FROM N.A.
 RA Dvorachek W.H., Natvig D.N.;
 RT "Characterization of sod-2, the Neurospora crassa gene for manganese
 superoxide dismutase.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 SEQUENCE FROM N.A.
 RC STRAIN=74-OR23-1A / FGSC 987;
 RX MEDLINE=22542210; PubMed=12655011;
 RA Mannhaupt G., Montrone C., Haase D., Mewes H.-W., Aign V.,
 RA Hoheisel J.D., Fartmann B., Nyakatura G., Kempken F., Maier J.,
 RA Schulte U.;
 RT "What's in the genome of a filamentous fungus? Analysis of the
 Neurospora genome sequence.";
 RL Nucleic Acids Res. 31:1944-1954(2003).
 CC -!- FUNCTION: Destroys radicals which are normally produced within the
 cells and which are toxic to biological systems.
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
 CC -!- SUBUNIT: Homotetramer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
 CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
 family.

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 EMBL; AF118809; AAD28503.1; -;
 DR EMBL; AL670011; CAD21408.1; -;
 DR HSSP; P04179; 1AEM.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe; 1.
 DR Pfam; PF02777; sodfe; 1.
 DR PRINTS; PR01703; MNSODISMUTASE.
 DR PRODOM; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD_MN; 1.
 KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
 KW Transit peptide.
 FT TRANSIT 1 32 MITOCHONDRION (POTENTIAL).
 FT CHAIN 33 245 SUPEROXIDE DISMUTASE [MN].
 FT METAL 58 58 MANGANESE (BY SIMILARITY).
 FT METAL 106 106 MANGANESE (BY SIMILARITY).
 FT METAL 196 196 MANGANESE (BY SIMILARITY).
 FT METAL 200 200 MANGANESE (BY SIMILARITY).
 SQ SEQUENCE 245 AA; 27019 MW; FF288947FB7676AD CRC64;
 Query Match 57.2%; Score 83; DB 1; Length 245;
 Best Local Similarity 55.6%; Pred. No. 5.2e-05;
 Matches 15; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 QY 2 YSLPELDVEFSATEPYISQINEIXY 28
 DB 34 YSLPOLPAYNALEPYISQIMELHHS 60


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RESULT 14
SODM RABIT
ID SODM RABIT STANDARD; PRT; 202 AA.
AC P41982;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1)
DE (Fragment).
GN SOD2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=New Zealand white;
RC Jackson R.M.;
RA Submitted (XXX-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC
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CC
DR EMBL; L28808; AAA31401.1; -.
DR HSSP; P04179; 1AP6.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sofde; 1.
DR Pfam; PF02777; sofde; C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
KW Transit peptide.
FT NON_TER 1 5 MITOCHONDRION (BY SIMILARITY).
FT TRANSIT <1 6 >202 SUPEROXIDE DISMUTASE [MN].
FT CHAIN 31 31 MANGANESE (BY SIMILARITY).
FT METAL 79 79 MANGANESE (BY SIMILARITY).
FT METAL 164 164 MANGANESE (BY SIMILARITY).
FT METAL 168 168 MANGANESE (BY SIMILARITY).
FT NON_TER 202 202 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 202 AA; 22656 MW; 6F1BB8DA15C33AA7 CRC64;

Query Match 53.1%; Score 77; DB 1; Length 202;
Best Local Similarity 46.4%; Pred. No. 0.00033;
Matches 13; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYFSAPEYVIGQINEIXYT 28
DB 6 KHSPLDPLDYGALEPHINAQIMELHHS 33

RESULT 15
SODF_METU
ID SODF_METU STANDARD; PRT; 202 AA.
AC P23744;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn/Fe] (EC 1.15.1.1).

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GN SODB.
OS Methylobionas J.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;
OC Methylococcaceae; Methylobionas.
OX NCBI_TaxID=32038;
RN [1]
RN SEQUENCE.
RP MEDLINE=91182736; PubMed=1848999;
RA Matsumoto T., Terauchi K., Isobe T., Matsuo K., Yamakura F.;
RT "Iron- and manganese-containing superoxide dismutases from
RT Methylobionas J.: identity of the protein moiety and amino acid
RT sequence."
RL Biochemistry 30:3210-3216 (1991).
RN [2]
RP CHARACTERIZATION, AND SEQUENCE OF 1-32.
RX MEDLINE=91301511; PubMed=1906419;
RA Yamakura F., Matsumoto T., Terauchi K.;
RT "Isolation of Mn-SOD and low active Fe-SOD from Methylobionas J;
RT consisting of identical proteins."
RL Free Radic. Res. Commun. 12:329-334 (1991).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese or iron ion per subunit (By
CC similarity).
CC -!- SUBUNIT: Homodimer.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC
DR HSSP; P00448; 1VEW.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sofde; 1.
DR Pfam; PF02777; sofde; C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
KW Oxidoreductase; Metal-binding; Manganese; Iron.
FT METAL 26 26 MANGANESE OR IRON (BY SIMILARITY).
FT METAL 80 80 MANGANESE OR IRON (BY SIMILARITY).
FT METAL 163 163 MANGANESE OR IRON (BY SIMILARITY).
FT METAL 167 167 MANGANESE OR IRON (BY SIMILARITY).
SQ SEQUENCE 202 AA; 22363 MW; 3213A8B4697A5B58 CRC64;

Query Match 52.4%; Score 76; DB 1; Length 202;
Best Local Similarity 51.9%; Pred. No. 0.00047;
Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 2 YSLPELDYFSAPEYVIGQINEIXYT 28
DB 2 YLPLPDYATALEPHIDAQTWEIHT 28

RESULT 16
SODM_CALJA
ID SODM_CALJA STANDARD; PRT; 198 AA.
AC Q8HYE0;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1).
GN SOD2.
OS Callitrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
OC Callitrix.
OX NCBI_TaxID=9483;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=22271545; PubMed=12383507;
RA Fukuhara R., Tezuka T., Kageyama T.;
RT "Structure, molecular evolution, and gene expression of primate
RT superoxide dismutases."
RL Gene 296:99-109 (2002).
CC -!- FUNCTION: Destroys radicals which are normally produced within the

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CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC
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CC
CC EMBL: AB087281; BAC20360.1; ALT INIT.
CC InterPro: IPR001189; SODismutase.
CC Pfam: PF00081; sodfe, 1.
CC PRINTS: PR01703; MNSODISMUTASE.
CC PROSITE: PD000475; SODismutase; 1.
CC OXIDOREDUCTASE: Metal-binding; Manganese; Mitochondrion.
CC METAL 26 26 MANGANESE (BY SIMILARITY).
CC METAL 74 74 MANGANESE (BY SIMILARITY).
CC METAL 159 159 MANGANESE (BY SIMILARITY).
CC METAL 163 163 MANGANESE (BY SIMILARITY).
CC SEQUENCE 198 AA; 22248 MW; E7F8860B8C56F2CA CRC64;
CC
CC Query Match 51.0%; Score 74; DB 1; Length 198;
CC Best Local Similarity 42.9%; Pred. No. 0.0009;
CC Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
CC
CC QY 1 KYSLPELDYFSAPEYISQINEIXYT 28
CC Db 1 KHSPLDPLPYDYGALPHINAQIMQLHHS 28
CC
CC RESULT 18
CC SODM_HYLLA STANDARD; PRT; 198 AA.
CC ID SODM_HYLLA STANDARD; PRT; 198 AA.
CC AC Q8HXP5;
CC DT 15-MAR-2004 (Rel. 43, Created)
CC DT 15-MAR-2004 (Rel. 43, Last sequence update)
CC DT 15-MAR-2004 (Rel. 43, Last annotation update)
CC DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1).
CC GN SOD2.
CC OS Hylobates lar (Common gibbon).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
CC OX NCBI_TaxID=9580;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=22271545; PubMed=12383507;
CC RA Fukuhara R., Tezuka T., Kageyama T.;
CC RT "Structure, molecular evolution, and gene expression of primate
CC RT superoxide dismutases."
CC RL Gene 296:99-109(2002).
CC CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC CC cells and which are toxic to biological systems.
CC CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC CC -!- SUBUNIT: Homotetramer (By similarity).
CC CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC CC family.
CC
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CC
CC EMBL: AB087276; BAC20355.1; ALT INIT.
CC InterPro: IPR001189; SODismutase.
CC Pfam: PF00081; sodfe, 1.
CC PRINTS: PR01703; MNSODISMUTASE.
CC PROSITE: PD000475; SODismutase; 1.
CC OXIDOREDUCTASE: Metal-binding; Manganese; Mitochondrion.
CC METAL 26 26 MANGANESE (BY SIMILARITY).
CC METAL 74 74 MANGANESE (BY SIMILARITY).
CC SEQUENCE 198 AA; 22248 MW; E7F8860B8C56F2CA CRC64;
CC
CC Query Match 51.0%; Score 74; DB 1; Length 198;
CC Best Local Similarity 42.9%; Pred. No. 0.0009;
CC Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
CC
CC QY 1 KYSLPELDYFSAPEYISQINEIXYT 28
CC Db 1 KHSPLDPLPYDYGALPHINAQIMQLHHS 28
CC
CC RESULT 17
CC SODM_CEBAP STANDARD; PRT; 198 AA.
CC ID SODM_CEBAP STANDARD; PRT; 198 AA.
CC AC Q8HXP1;
CC DT 15-MAR-2004 (Rel. 43, Created)
CC DT 15-MAR-2004 (Rel. 43, Last sequence update)
CC DT 15-MAR-2004 (Rel. 43, Last annotation update)
CC DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1).
CC GN SOD2.
CC OS Cebus apella (Brown-capped capuchin).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus.
CC OX NCBI_TaxID=9515;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=22271545; PubMed=12383507;
CC RA Fukuhara R., Tezuka T., Kageyama T.;
CC RT "Structure, molecular evolution, and gene expression of primate
CC RT superoxide dismutases."
CC RL Gene 296:99-109(2002).
CC CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC CC cells and which are toxic to biological systems.
CC CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC CC -!- SUBUNIT: Homotetramer (By similarity).
CC CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC CC family.
CC
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


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CC -----
DR EMBL; AB087275; BAC20354.1; ALT INIT.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR Pfam; PF02777; sodfe; C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
DR Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
FT METAL 26 26 MANGANESE (BY SIMILARITY).
FT METAL 74 74 MANGANESE (BY SIMILARITY).
FT METAL 159 159 MANGANESE (BY SIMILARITY).
FT METAL 163 163 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 198 AA; 22204 MW; F772RABBA6A9F4CD CRC64;

Query Match 51.0%; Score 74; DB 1; Length 198;
Best Local Similarity 42.9%; Pred. No. 0.0009;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYFESATPEYISQINEIXYT 28
D 1 KHSPLDLPYDGALEPHINAQIMQLHHS 28
D 1 KHSPLDLPYDGALEPHINAQIMQLHHS 28

RESULT 24
SODF_ACIAM STANDARD; PRT; 211 AA.
AC Q9P9T3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Fe] (EC 1.15.1.1).
GN SOD.
OS Acidianus ambivalens (Desulfurolobus ambivalens).
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Acidianus.
OX NCBI_TaxID=2283;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21026956; PubMed=11154067;
RA Kardinahl S., Anemuller S., Schaefer G.;
RT "The hyper-thermostable Fe-superoxide dismutase from the Archaeon
RT Acidianus ambivalens: characterization, recombinant expression,
RT crystallization and effects of metal exchange.";
RL Biol. Chem. 381:1089-1101(2000).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems (By similarity).
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 iron ion per subunit (By similarity).
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC -----
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CC -----
CC EMBL; AF236110; AAF36989.1; -.
CC HSP; P80857; 1SSS.
CC InterPro; IPR001189; SODismutase.
CC Pfam; PF00081; sodfe; 1.
CC Pfam; PF02777; sodfe; C; 1.
CC PRINTS; PR01703; MNSODISMUTASE.
CC ProDom; PD000475; SODismutase; 1.
CC PROSITE; PS00088; SOD_MN; FALSE NEG.
CC Oxidoreductase; Metal-binding; Iron.
FT METAL 34 34 IRON (BY SIMILARITY).
FT METAL 82 82 IRON (BY SIMILARITY).
FT METAL 171 171 IRON (BY SIMILARITY).
FT METAL 175 175 IRON (BY SIMILARITY).

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SQ SEQUENCE 211 AA; 24342 MW; 5A88FFE400F77065 CRC64;

Query Match 51.0%; Score 74; DB 1; Length 211;
Best Local Similarity 51.9%; Pred. No. 0.00097;
Matches 14; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 KYSLPELDYFESATPEYISQINEIXY 27
D 9 KYELPPLPYNDALPEYISKEIIDVHY 35
D 9 KYELPPLPYNDALPEYISKEIIDVHY 35

RESULT 25
SODM_BOVIN STANDARD; PRT; 222 AA.
ID SODM_BOVIN
AC P41976;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
GN SOD2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=94121934; PubMed=8292376;
RA Meyrick B., Magnuson M.A.;
RT "Identification and functional characterization of the bovine
RT manganous superoxide dismutase promoter.";
RL Am. J. Respir. Cell Mol. Biol. 10:113-121(1994).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L22092; AAA30655.1; ALT_INIT.
CC EMBL; L22093; AAA30656.1; -.
CC EMBL; S67818; AAC60522.2; -.
CC EMBL; S67819; AADI4001.1; -.
CC PIR; I51918; I51918.
CC HSP; P04179; IABW.
CC InterPro; IPR001189; SODismutase.
CC Pfam; PF00081; sodfe; 1.
CC Pfam; PF02777; sodfe; C; 1.
CC PRINTS; PR01703; MNSODISMUTASE.
CC ProDom; PD000475; SODismutase; 1.
CC PROSITE; PS00088; SOD_MN; 1.
CC Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
CC Transit peptide.
FT TRANSIT 1 24 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 25 222 SUPEROXIDE DISMUTASE [MN].
FT METAL 50 50 MANGANESE (BY SIMILARITY).
FT METAL 98 98 MANGANESE (BY SIMILARITY).
FT METAL 183 183 MANGANESE (BY SIMILARITY).
FT METAL 187 187 MANGANESE (BY SIMILARITY).
FT CONFLICT 8 8 S -> R (IN REF. 1; AADI4001).
FT CONFLICT 90 90 F -> V (IN REF. 1; AAC60522).
SQ SEQUENCE 222 AA; 24638 MW; 806CC3FCBIA74413 CRC64;

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Query Match 51.0%; Score 74; DB 1; Length 222;
 Best Local Similarity 42.9%; Pred. No. 0.001;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSTATPEYISQINEIXVT 28
 Db 25 KHSPLDLPDYGALEPHINQIMQLHHS 52

RESULT 26

SODM HUMAN
 ID SODM HUMAN STANDARD; PRT; 222 AA.
 AC P04179; P78434; Q16792; Q9P223;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
 GN SOD2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89076921; PubMed=2462451;
 RA Wispe J.R., Clark J.C., Burhans M.S., Kropp K.E., Korfhagen T.R.,
 RA Whitsett J.A.;
 RT "Synthesis and processing of the precursor for human
 RT mangano-superoxide dismutase.";
 RL Biochim. Biophys. Acta 994:30-36(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88067716; PubMed=3684581;
 RA Beck Y., Oren R., Amit B., Levanon A., Gorecki M., Hartman J.R.;
 RT "Human Mn superoxide dismutase cDNA sequence.";
 RL Nucleic Acids Res. 15:9076-9076(1987).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANT VAL-16.
 RX MEDLINE=88289364; PubMed=339391;
 RA Heckl K.;
 RT "Isolation of cDNAs encoding human manganese superoxide dismutase.";
 RL Nucleic Acids Res. 16:6224-6224(1988).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88152250; PubMed=2831093;
 RA Ho Y.-S., Crapo J.D.;
 RT "Isolation and characterization of complementary DNAs encoding human
 RT manganese-containing superoxide dismutase.";
 RL FEBS Lett. 229:256-260(1988).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RX MEDLINE=91105727; PubMed=1988135;
 RA St Clair D.K., Holland J.C.;
 RT "Complementary DNA encoding human colon cancer manganese superoxide
 RT dismutase and the expression of its gene in human cells.";
 RL Cancer Res. 51:939-943(1991).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91027939; PubMed=1699607;
 RA Church S.L.;
 RT "Manganese superoxide dismutase: nucleotide and deduced amino acid
 RT sequence of a cDNA encoding a new human transcript.";
 RL Biochim. Biophys. Acta 1087:250-252(1990).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95217333; PubMed=7702755;
 RA Wan X.S., Devalaraja M.N., St Clair D.K.;
 RT "Molecular structure and organization of the human manganese
 RT superoxide dismutase gene.";
 RL DNA Cell Biol. 13:1127-1136(1994).

RN [8]
 RP SEQUENCE OF 25-222.
 RX MEDLINE=85030346; PubMed=6386798;
 RA Barra D., Schinina M.E., Simmaco M., Bannister J.V., Bannister W.H.,
 RA Rotilio G., Bossa F.;
 RT "The primary structure of human liver manganese superoxide
 RT dismutase.";
 RL J. Biol. Chem. 259:12595-12601(1984).
 RN [9]
 RP SEQUENCE OF 25-39.
 RC TISSUE=Heart;
 RX MEDLINE=95203287; PubMed=7895732;
 RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
 RT "The human myocardial two-dimensional gel protein database: update
 RT 1994.";
 RL Electrophoresis 15:1459-1465(1994).
 RN [10]
 RP SEQUENCE OF 25-39.
 RC TISSUE=Heart;
 RX MEDLINE=96007936; PubMed=7498159;
 RA Kovalyov L.I., Shishkin S.S., Bfimochkin A.S., Kovalyova M.A.,
 RA Eshnova E.S., Egorov T.A., Masalyanov A.K.;
 RT "The major protein expression profile and two-dimensional protein
 RT database of human heart.";
 RL Electrophoresis 16:1160-1169(1995).
 RN [11]
 RP SEQUENCE OF 25-39.
 RC TISSUE=Breast carcinoma;
 RX MEDLINE=97295304; PubMed=9150946;
 RA Rasmussen R.K., Ji H., Eddes J.S., Moritz R.L., Reid G.E.,
 RA Simpson R.J., Dorow D.S.;
 RT "Two-dimensional electrophoretic analysis of human breast carcinoma
 RT proteins: mapping of proteins that bind to the SH3 domain of mixed
 RT lineage kinase MLK2.";
 RL Electrophoresis 18:588-598(1997).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=93008233; PubMed=1394426;
 RA Borgstahl G.E.O., Parge H.E., Hickey M.J., Beyer W.F. Jr.,
 RA Hallewell R.A., Tainer J.A.;
 RT "The structure of human mitochondrial manganese superoxide dismutase
 RT reveals a novel tetrameric interface of two 4-helix bundles.";
 RL Cell 71:107-118(1992).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF VARIANT THR-82.
 RX MEDLINE=96183289; PubMed=8605177;
 RA Borgstahl G.E.O., Parge H.E., Hickey M.J., Johnson M.J.,
 RA Boissinot M., Hallewell R.A., Lepock J.R., Cabelli D.E.,
 RA Tainer J.A.;
 RT "Human mitochondrial manganese superoxide dismutase polymorphic
 RT variant Ile58Thr reduces activity by destabilizing the tetrameric
 RT interface.";
 RL Biochemistry 35:4287-4297(1996).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF VARIANT ASN-167.
 RX MEDLINE=98206888; PubMed=9537988;
 RA Hsieh Y., Guan Y., Tu C., Bratt P.J., Angerhofer A., Lepock J.R.,
 RA Hickey M.J., Tainer J.A., Nick H.S., Silverman D.N.;
 RT "Probing the active site of human manganese superoxide dismutase: the
 RT role of glutamine 143.";
 RL Biochemistry 37:4731-4739(1998).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF VARIANT TYR-58.
 RX MEDLINE=98206887; PubMed=9537987;
 RA Guan Y., Hickey M.J., Borgstahl G.E.O., Hallewell R.A., Lepock J.R.,
 RA O'Connor D., Hsieh Y., Nick H.S., Silverman D.N., Tainer J.A.;
 RT "Crystal structure of Y34F mutant human mitochondrial manganese
 RT superoxide dismutase and the functional role of tyrosine 34.";
 RL Biochemistry 37:4722-4730(1998).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (2.13 ANGSTROMS) OF MUTANT ALA-167.
 RX MEDLINE=20311275; PubMed=10852710;
 RA Leveque V.J.-P., Stroupe M.E., Lepock J.R., Cabelli D.E., Tainer J.A.,

FT	CONFLICT	138	138	V -> M (IN REF. 1 AND 3).
SQ	SEQUENCE	222 AA;	24603 MW;	9AE804C55A8357D9 CRC64;
	Query Match	51.0%	Score 74;	DB 1;
	Best Local Similarity	42.9%	Pred. No. 0.001;	Length 222;
	Matches 12;	Conservative 10;	Mismatches 6;	Indels 0;
	Gaps 0;			
QY	1 KYSLEPDIYFSATPYISGGQINEIXYT 28			
Db	25 KHSLPDLPDYGALEPHINAQIMQLHHS 52			
	RESULT 28			
SODM	RAT	STANDARD;	PRT;	222 AA.
ID	SODM RAT			
AC	P07895;			
DT	01-AUG-1988 (Rel. 08, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).			
GN	SOD2.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley; TISSUE=Liver;			
RX	MEDLINE=88096516; PubMed=3697077;			
RA	Ho Y.-S., Crapo J.D.;			
RT	"Nucleotide sequences of cDNAs coding for rat manganese-containing superoxide dismutase.";			
RT	Nucleic Acids Res. 15:10070-10070(1987).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley; TISSUE=Liver;			
RX	MEDLINE=91159005; PubMed=2001291;			
RA	Ho Y.-S., Howard A.J., Crapo J.D.;			
RT	"Molecular structure of a functional rat gene for manganese-containing superoxide dismutase.";			
RT	Am. J. Respir. Cell Mol. Biol. 4:278-286(1991).			
CC	-I- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.			
CC	-I- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).			
CC	-I- COFACTOR: Binds 1 manganese ion per subunit (By similarity).			
CC	-I- SUBUNIT: Homotetramer.			
CC	-I- SUBCELLULAR LOCATION: Mitochondrial matrix.			
CC	-I- SIMILARITY: Belongs to the iron/manganese superoxide dismutase family.			
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DR	EMBL; Y00497; CAA68549.1; -			
DR	EMBL; X56600; CAA39937.1; -			
DR	PIR; S21661; DSFTN.			
DR	HSSP; P04179; IABM.			
DR	InterPro; IPR001189; SODismutase.			
DR	Pfam; PF00081; sodfe; 1.			
DR	Pfam; PF02777; sodfe; 1.			
DR	PRINTS; PR01703; MNSODISMUTASE.			
DR	ProDom; PD000475; SODismutase; 1.			
DR	PROSITE; PS00088; SOD_MN; 1.			
DR	Oxidoreductase; Metal-binding; Manganese; Mitochondrion; Transit peptide.			
FT	TRANSIT	1	24	MITOCHONDRION.
FT	CHAIN	25	222	SUPEROXIDE DISMUTASE [MN].
FT	METAL	50	50	MANGANESE (BY SIMILARITY).
FT	CONFLICT	18	18	G -> V (IN REF. 5; AAH18173).
FT	CONFLICT	18	18	G -> V (IN REF. 1 AND 3).

```

FT METAL 98 98 MANGANESE (BY SIMILARITY) .
FT METAL 183 183 MANGANESE (BY SIMILARITY) .
FT METAL 187 187 MANGANESE (BY SIMILARITY) .
FT CONFLICT 167 167 Q -> H (IN REF. 1) . CRC64;
SQ SEQUENCE 222 AA; 24674 MW; 8CCCE05857B3138 CRC64;

Query Match 51.0%; Score 74; DB 1; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.001;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSSATEPYISQINEIXY 28
DB 25 KHSLEPDLFYDYGALPHINAQIMQLHHS 52

RESULT 29
SODF_SULSO STANDARD; PRT; 210 AA.
AC P80857;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Fe] (EC 1.15.1.1).
GN SOD OR SSO0316.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE.
RC STRAIN=ATCC 49255 / DSM 5833 / MT-4;
RX MEDLINE=99098843; PubMed=9880816;
RA Yamano S., Maruyama T.;
RT "An azide-insensitive superoxide dismutase from a hyperthermophilic
archaeon, Sulfolobus solfataricus."
RL J. Biochem. 125:186-193(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49255 / DSM 5833 / MT-4;
RX MEDLINE=21145482; PubMed=11248699;
RA De Vendittis E., Ursby T., Rullo R., Gogliettino M.A., Masullo M.,
RA Bocchini V.;
RT "Phenylmethanesulfonyl fluoride inactivates an archaeal superoxide
dismutase by chemical modification of a specific tyrosine residue:
cloning, sequencing and expression of the gene coding for Sulfolobus
solfataricus superoxide dismutase."
RL Eur. J. Biochem. 268:1794-1801(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Awayez M.J., Chan-Weher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Erasuo G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Senses C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2."
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=99134398; PubMed=9931259;
RA Ursby T., Adinolfi B.S., Al-Karadaghi S., de Vendittis E.,
RA Bocchini V.;

```

```

RT FT
RT FT
RL J. Mol. Biol. 286:189-205(1999).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 iron ion per subunit.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC
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CC
CC EMBL; AB012620; BAA75509.1; -.
DR EMBL; Y15326; CAA75583.1; -.
DR EMBL; AE006666; AAK40652.1; -.
DR PIR; E90174; E90174.
DR PDB; 1SSS; 09-APR-99.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodef, 1.
DR Pfam; PF02777; sodef, 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; FALSE NEG.
DR Oxidoreductase; Metal-binding; Iron; 3D-structure; Complete proteome.
KW INIT_MET 0 0
FT METAL 37 37 IRON.
FT METAL 84 84 IRON.
FT METAL 170 170 IRON.
FT METAL 174 174 IRON.
FT TURN 18 24
FT HELIX 27 35
FT TURN 36 36
FT TURN 37 57
FT TURN 58 58
FT TURN 62 63
FT HELIX 67 89
FT TURN 90 90
FT STRAND 91 91
FT STRAND 94 94
FT TURN 95 96
FT STRAND 97 97
FT HELIX 103 113
FT HELIX 116 129
FT STRAND 134 140
FT TURN 142 144
FT STRAND 147 153
FT TURN 154 156
FT STRAND 157 157
FT STRAND 165 170
FT HELIX 173 175
FT TURN 176 176
FT HELIX 177 180
FT TURN 181 182
FT HELIX 184 191
FT STRAND 192 194
FT STRAND 195 195
FT HELIX 197 206
FT TURN 207 207
SQ SEQUENCE 210 AA; 24112 MW; 7918CF1292BF98B6 CRC64;

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Query Match 50.3%; Score 73; DB 1; Length 210;
Best Local Similarity 51.9%; Pred. No. 0.0014;
Matches 14; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSSATEPYISQINEIXY 27


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OX NCB1_TaxID=5085;
RP [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 42202 / AF-102;
RX MEDLINE=96305209; PubMed=9691141;
RA Cramer R., Faith A., Hemmann S., Jaussi R., Ismail C., Menz G.,
RA Blaser K.;
RT "Humoral and cell-mediated autoimmunity in allergy to Aspergillus
RT fumigatus.";
RL J. Exp. Med. 184:265-270 (1996).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=21659899; PubMed=11801664;
RA Gruetiger S., Mittel P.R.B., Scapozza L., Fijten H., Folkers G.,
RA Fluettiger M.G., Blaser K., Cramer R.;
RT "Comparison of the crystal structures of the human manganese
RT superoxide dismutase and the homologous Aspergillus fumigatus
RT allergen at 2-A resolution.";
RL J. Immunol. 168:1267-1272 (2002).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Binds 1 manganese ion per subunit.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- ALLERGEN: Causes an allergic reaction in human.
CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC
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CC
CC -----
DR EMBL; U53561; AAB60779.1; ALT_INIT.
DR FDB; 1KKC; 30-JAN-02.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR PRINTS; PR01703; sodfe; 1.
DR PROSITE; PR01703; MNSODISMASE.
DR PROSITE; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
DR Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
KW Transit peptide; Allergen; 3D-structure.
FT CHAIN 1 ? MITOCHONDRION (BY SIMILARITY).
FT METAL 29 29 SUPEROXIDE DISMUTASE [MN].
FT METAL 77 77 MANGANESE.
FT METAL 163 163 MANGANESE.
FT METAL 167 167 MANGANESE.
SQ SEQUENCE 210 AA; 23377 MW; CE64A134780E5546 CRC64;

Query Match 49.0%; Score 71; DB 1; Length 210;
Best Local Similarity 48.1%; Pred. No. 0.0027;
Matches 13; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSAATEPYISQINEIXY 27
DB 4 QITLPLPYDQALQFYISQIMELHH 30

RESULT 33
SODM_HEVER
ID SODM_HEVER STANDARD; PRT; 233 AA.
AC P35017;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
GN SODA.
OS Hevea brasiliensis (Para rubber tree).

```

```

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae; Micrandreae;
OC Hevea.
OX NCB1_TaxID=3981;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=94033306; PubMed=8219064;
RA Miao Z., Gaynor J.J.;
RT "Molecular cloning, characterization and expression of Mn-superoxide
RT dismutase from the rubber tree (Hevea brasiliensis).";
RL Plant Mol. Biol. 23:267-277 (1993).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- TISSUE SPECIFICITY: Present in all tissues examined (leaf,
CC petiole, root, latex, callus) with young leaves showing the
CC highest levels in intact plants.
CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC
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CC
CC -----
DR EMBL; L11707; AAA16792.1; -.
DR FIR; S39492; S39492.
DR HSSP; P04179; IABM.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR PRINTS; PR01703; sodfe; 1.
DR PROSITE; PR01703; MNSODISMASE.
DR PROSITE; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
DR Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
KW Transit peptide.
FT CHAIN 1 27 MITOCHONDRION (BY SIMILARITY).
FT METAL 28 233 SUPEROXIDE DISMUTASE [MN].
FT METAL 59 59 MANGANESE (BY SIMILARITY).
FT METAL 103 103 MANGANESE (BY SIMILARITY).
FT METAL 192 192 MANGANESE (BY SIMILARITY).
FT METAL 196 196 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 233 AA; 25839 MW; D6C48D7A7E9A8D59 CRC64;

Query Match 49.0%; Score 71; DB 1; Length 233;
Best Local Similarity 46.2%; Pred. No. 0.003;
Matches 12; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSAATEPYISQINEIXY 27
DB 31 FSLPDLPYDYGALPAISGIMQLHH 56

RESULT 34
SODM_BORBU
ID SODM_BORBU STANDARD; PRT; 203 AA.
AC O30563;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Fe] (EC 1.15.1.1).
GN SOD OR BB0153.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCB1_TaxID=139;

```


[illegible]

GN SODA.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]_SEQUENCE FROM N.A.
RP TISSUE=Leaf;
RC MEDLINE=92032795; PubMed=1932701;
RA Wong-Vega L., Burke J.J., Allen R.D.;
RX "Isolation and sequence analysis of a cDNA that encodes pea manganese
superoxide dismutase.";
RL Plant Mol. Biol. 17:1271-1274 (1991).
RN [2]
RP REVISIONS.
RC SPRAIN=cv. Alaska; TISSUE=Etolated bud;
RA Jaradat T., Wong-Vega L., Allen R.D.;
RX Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RL
CC -!- FUNCTION: Destroys radicals which are normally produced within the
cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
family.
CC
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CC
CC -----
CC EMBL; X60170; CAA42737.1; -;
CC EMBL; U30841; AAA74442.1; -;
CC PIR; S18343; DSPMN.
CC HSPSP; P04179; IABM.
CC InterPro: IPR001189; SODismutase.
CC Pfam; PF02777; sodfe; 1.
CC Pfam; PF02777; sodfe; 1.
CC PRINTS; PR01703; MNSODISMUTASE.
CC ProDom; PD000475; SODismutase; 1.
CC PROSITE; PS00088; SOD_MN; 1.
CC Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
KW Transit peptide.
KW TRANSIT 1 36 MITOCHONDRION (PROBABLE).
FT CHAIN 37 233 SUPEROXIDE DISMUTASE [MN].
FT METAL 64 64 MANGANESE (BY SIMILARITY).
FT METAL 112 112 MANGANESE (BY SIMILARITY).
FT METAL 194 194 MANGANESE (BY SIMILARITY).
FT METAL 198 198 MANGANESE (BY SIMILARITY).
FT CONFLICT 160 160 Q -> QASGW (IN REF. 1).
FT CONFLICT 176 176 T -> TAN (IN REF. 1).
FT CONFLICT 192 192 G -> W (IN REF. 1).
SQ SEQUENCE 233 AA; 25822 MW; DB246D1FF0AF4FF9 CRC64;
Query Match 48.3%; Score 70; DB 1; Length 233;
Best Local Similarity 46.2%; Pred. No. 0.0042;
Matches 12; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Oy 2 YSLPELYEFSATPEYISGQNEIXY 27
Db 40 FTLPDLAYDYGALEPVISGEIMQIH 65

RESULT 38
SODF_BACSU STANDARD; PRT; 281 AA.
AC O35023;
DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable superoxide dismutase [Fe] (EC 1.15.1.1).
GN SODF OR BSU19330.
GN Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]_SEQUENCE FROM N.A.
RP Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;
RX "Sequence analysis of the Bacillus subtilis chromosome region between
the terC and ochaB loci cloned in a yeast artificial chromosome.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Berteiro M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerion I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Etian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Giseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaer-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Pressecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche E., Rose M., Sadale I.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenberg M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
subtilis.";
RL Nature 390:249-256 (1997).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 iron ion per subunit (By similarity).
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
family.
CC
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CC
CC -----
CC EMBL; AF027868; AAB84442.1; -;
CC EMBL; Z99114; CAB13825.1; -;
CC PIR; C69709; C69709.
CC HSSP; P80293; IABM.
CC Subtilist; BG12676; sodf.
CC InterPro: IPR001189; SODismutase.
CC Pfam; PF00081; sodfe; 1.
CC Pfam; PF02777; sodfe; 1.
CC PRINTS; PR01703; MNSODISMUTASE.
CC ProDom; PD000475; SODismutase; 1.
CC PROSITE; PS00088; SOD_MN; 1.
CC Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
KW Transit peptide.
KW TRANSIT 1 36 MITOCHONDRION (PROBABLE).
FT CHAIN 37 233 SUPEROXIDE DISMUTASE [MN].
FT METAL 64 64 MANGANESE (BY SIMILARITY).
FT METAL 112 112 MANGANESE (BY SIMILARITY).
FT METAL 194 194 MANGANESE (BY SIMILARITY).
FT METAL 198 198 MANGANESE (BY SIMILARITY).
FT CONFLICT 160 160 Q -> QASGW (IN REF. 1).
FT CONFLICT 176 176 T -> TAN (IN REF. 1).
FT CONFLICT 192 192 G -> W (IN REF. 1).
SQ SEQUENCE 233 AA; 25822 MW; DB246D1FF0AF4FF9 CRC64;

Qy	4 LPELDYEFSATEPYISQINEIXY 27
	: : : :
Db	5 LPDLPAYDALEPYISRQIMELHH 28

Search completed: August 24, 2004, 23:01:02
Job time : 24 secs

R;Accession: S06599; A37212
C;Rhangaraj, H.S.; Lamb, F.I.; Davis, E.O.; Colston, M.J.
Nucleic Acids Res. 17, 8378, 1989
A;Title: Nucleotide and deduced amino acid sequence of *Mycobacterium leprae* manganese superoxide dismutase
A;Reference number: S06599; MUID:90045970; PMID:2682526
A;Accession: S06599
A;Molecule type: DNA

A; Residues: 1-207 <THA>
A; Cross-references: EMBL: X16453; NID: g44405; PID: g581343
R; Thangaraj, H.S.; Lamb, F.I.; Davis, E.O.; Jenner, P.J.; Jeyakumar, L.H.; Colston, M.J.
Infect. Immun. 58, 1937-1942, 1990
A; Title: Identification, sequencing, and expression of Mycobacterium leprae superoxide d
A; Reference number: A37212; NUID: 90256282; PMID: 1692812

A;Accession: A37212
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 'V', 2-207 <TH2>
A;Cross-references: GB:X16453
C;Genetics:

C; Gene: *per1*
A; Start codon: GTG
C; Function:
A; Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C; Superfamily: superoxide dismutase (Mn)
C; Keywords: manganese; metalloprotein; oxidoreductase
F; 28,76,160/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match	67.6%	Score 98	DB 2	Length 207
Best Local Similarity	57.1%	Pred. No. 2.9e-07		
Matches 15	Conservative 10	Mismatches 2	Indels 0	Gaps 0

Qy		1	KYSLPELDYEFSEATERYISGQINEIXYT	28
		:	: :: :: :: :: :: ::	
Dd		3	EYTLPLDLWDYAALPHISGRINEIHHT	30

RESULT 5
S15205
superoxide dismutase (EC 1.15.1.1) (Fe) [validated] - Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 21-Nov-1993 #sequence revision 26-May-1995 #text_change 20-Jun-2000
C;Accession: S15205; C79654; S10908
R;Zhang Y.; Lathigra R.; Garbe T.; Catty D.; Young, D.
Mol Microbiol 5:381-391 1991

Mol. Microbiol. 5, 481-491, 1991
 A>Title: Genetic analysis of superoxide dismutase, the 23 kilodalton antigen of *Mycobacterium tuberculosis*
 A:Reference number: S15205; PMID:91251768; PMID:19041126
 A:Accession: S15205
 A:Molecule type: DNA
 A:Residues: 1-207 <ZHA>
 A:Cross-references: EMBL:X52861; NID:g794079; PIDN:CAA37042.1; PID:g581379
 A:Experimental source: strain H37Rv

[illegible]

A:Accession: U0654
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-207 <COL>

A: Experimental source: strain H37RV
R: Cooper, J.B.; McIntyre, K.; Wood, S.P.; Zhang, Y.; Young, D.
submitted to the Brookhaven Protein Data Bank, September 1994
ATCROSS-references: GB:Z83864; GB:AU123456; NID:95261667; FIUN:CA060220.1; FID:91761111

J. Mol. Biol. 235, 1156-1158, 1994
A; Title: Crystallisation and preliminary X-ray analysis of the iron-dependent superoxide
R; Cooper, J.B.; Driessen, H.P.C.; Wood, S.P.; Zhang, Y.; Young, D.
A; Reference number: A59029; MUID: 94118350; PMID: 8289318
A; Contents: annotation; X-ray crystallography

C:Genetics:
A:Gene: soda
A:Start codon: GTG
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: iron; metalloprotein; oxidoreductase; tetramer
F:2-28,76,160,164/Binding site: iron (His, His, Asp, His) #status experimental

Query Match 64.8%; Score 94; DB 2; Length 207;
Best Local Similarity 53.6%; Pred. No. 1.2e-06;
Matches 15; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 1 KYSLPELDYFSAATEPYISQINEIXYT 28
DB 3 EYTLPELDYDGALEPHISQINELHHS 30

RESULT 6
JC4396
superoxide dismutase (EC 1.15.1.1) (Fe/Mn) [validated] - Propionibacterium freudenreichii
C:Species: Propionibacterium freudenreichii subsp. shermanii
C:Date: 20-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 20-Apr-2000
C:Accession: JC4396; S41106
R:Gabbianelli, R.; Battistoni, A.; Polizio, F.; Carri, M.T.; De Martino, A.; Meier, B.; Biochem. Biophys. Res. Commun. 216, 841-847, 1995
A:Title: Metal uptake of recombinant cambialistic superoxide dismutase from Propionibacterium freudenreichii
A:Reference number: JC4396; MUID:96074560; PMID:7488202
A:Accession: JC4396
A:Molecule type: DNA
A:Residues: 1-202 <GAB>
A:Cross-references: EMBL:X91650
A:Experimental source: PZ3
R:Meier, B.; Sehn, A.P.; Schinina, M.E.; Barra, D. Eur. J. Biochem. 219, 463-468, 1994
A:Title: In vivo incorporation of copper into the iron-exchangeable and manganese-exchangeable superoxide dismutase
A:Reference number: S41106; MUID:94139724; PMID:8307013
A:Accession: S41106
A:Molecule type: protein
A:Residues: 2-202 <MEI>
A:Experimental source: strain PZ3
C:Genetics:
A:Gene: sod
C:Complex: homotetramer
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
A:Note: can use iron or manganese as cofactor
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: homotetramer; iron; manganese; metalloprotein; oxidoreductase
F:2-202/Product: superoxide dismutase #status experimental <MAT>
F:28,76,162,166/Binding site: iron/manganese (His, His, Asp, His) #status predicted

Query Match 62.8%; Score 91; DB 2; Length 202;
Best Local Similarity 61.5%; Pred. No. 3.2e-06;
Matches 16; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 YSLPELDYFSAATEPYISQINEIXY 27
DB 4 YTLPELDYDGALEPHISQINELHHS 29

RESULT 7
A38461
superoxide dismutase (EC 1.15.1.1) (Fe/Mn) - Methylobacterium sp.
C:Species: Methylobacterium sp.
C:Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 20-Apr-2000
C:Accession: A38461; A61532; B61532
R:Matsuoka, T.; Terauchi, K.; Isobe, T.; Matsuoka, K.; Yamakura, F. Biochemistry 30, 3210-3216, 1991
A:Title: Iron- and manganese-containing superoxide dismutases from Methylobacterium sp.
A:Reference number: A38461; MUID:91182736; PMID:1848999
A:Accession: A38461

A:Molecule type: protein
A:Residues: 1-202 <MAT>
R:Yamakura, F.; Matsuoka, T.; Terauchi, K. Free Radic. Res. Commun. 12, 329-334, 1991
A:Title: Isolation of Mn-SOD and low active Fe-SOD from Methylobacterium sp.
A:Reference number: A61532
A:Accession: A61532
A:Molecule type: protein
A:Residues: 1-332 <YAM>
A:Note: identical sequences were determined for Fe-SOD and Mn-SOD; these were shown in r
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: iron; manganese; metalloprotein; oxidoreductase
F:26,80,163,167/Binding site: iron/manganese (His, His, Asp, His) #status predicted

Query Match 52.4%; Score 76; DB 2; Length 202;
Best Local Similarity 51.9%; Pred. No. 0.0006;
Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 2 YSLPELDYFSAATEPYISQINEIXYT 28
DB 2 YTLPELDYDGALEPHISQINELHHS 28

RESULT 8
DSHUN
superoxide dismutase (EC 1.15.1.1) (Mn) precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 06-Feb-1995 #text_change 20-Apr-2000
C:Accession: S13162; S02272; S11756; S00356; S02230; S00663; A92447; I38033; A00520; A27
R:Church, S.L. Biochim. Biophys. Acta 1087, 250-252, 1990
A:Title: Manganese superoxide dismutase: nucleotide and deduced amino acid sequence of a
A:Reference number: S13162; MUID:91027939; PMID:1699607
A:Accession: S13162
A:Molecule type: mRNA
A:Residues: 1-222 <CHU>
A:Note: cross-reference GB:M34665 cited in paper is not correct
R:Wise, J.R.; Clark, J.C.; Burhans, M.S.; Kropp, K.E.; Korfhagen, T.R.; Whitsett, J.A. Biochim. Biophys. Acta 994, 30-36, 1989
A:Title: Synthesis and processing of the precursor for human manganese-superoxide dismutase
A:Reference number: S02272; MUID:89076921; PMID:2462451
A:Accession: S02272
A:Molecule type: mRNA
A:Residues: 1-81, 'T', 83-222 <WIS>
A:Cross-references: EMBL:X14322; NID:G34706; PIDN:CAA32502.1; PID:G34707
R:StClair, D.K.
submitted to the EMBL Data Library, April 1989
A:Description: Nucleotide sequence of a human tumor MnSOD cDNA.
A:Reference number: S11756
A:Accession: S11756
A:Molecule type: mRNA
A:Residues: 1-64, 'N', 66-222 <EMB>
A:Cross-references: EMBL:X15132; NID:G34794; PIDN:CAA33228.1; PID:G34795
R:Ho, Y.S.; Crapo, J.D. FEBS Lett. 229, 256-260, 1988
A:Title: Isolation and characterization of complementary DNAs encoding human manganese-c
A:Reference number: S00356; MUID:88152250; PMID:2831093
A:Accession: S00356
A:Molecule type: mRNA
A:Residues: 1-81, 'T', 83-222 <HO1>
A:Cross-references: EMBL:Y00985; NID:G36536; PIDN:CAA68791.1; PID:G36537
R:Heckl, K.
Nucleic Acids Res. 16, 6224, 1988
A:Title: Isolation of cDNAs encoding human manganese superoxide dismutase.
A:Reference number: S02230; MUID:88289364; PMID:3399391
A:Accession: S02230
A:Molecule type: mRNA
A:Residues: 1-13, 'P', 15, 'Y', 17-122, 'L', 124-222 <HEC>
A:Cross-references: EMBL:X07834; NID:G36517; PIDN:CAA30687.1; PID:G36518
A:Note: the authors translated the codon CTG for residue 123 as Arg
R:Beck, Y.; Oren, R.; Amit, B.; Levanon, A.; Gorecki, M.; Hartman, J.R.

F:25-222/Product: superoxide dismutase (Mn) #status predicted <MAT>
F:50,98,183,187/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 51.0%; Score 74; DB 2; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0014;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSAPEYISGQINEIXYT 28
DB 25 KHSPLDPLDYGALEPHINAIQMLHHS 52

RESULT 11

151918
superoxide dismutase (EC 1.15.1.1) (Mn) precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Oct-1996 #sequence revision 15-Aug-1997 #text_change 21-Jul-2000
C:Accession: I51918; I64848; I64850
R:Meyrick, B.; Magnuson, M.A.
A:Title: Identification and functional characterization of the bovine manganous superoxide dismutase
A:Reference number: I51918; MUID:94121934; PMID:8292376
A:Accession: I51918
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-222 <MEY1>
A:Cross-references: GB:L22092; NID:g498259; PIDN:AAA30655.1; PID:g498260
A:Accession: I64848
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7 <MEY2>
A:Cross-references: GB:L22093; NID:g498261; PIDN:AAA30656.1; PID:g552330
A:Accession: I64850
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7, 'R' <MEY3>
A:Cross-references: GB:S67819; NID:g460572; PIDN:AAD14001.1; PID:g4261701
C:Genetics:
A:Gene: MnSOD
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
F:1-24/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F:25-222/Product: superoxide dismutase (Mn) #status predicted <MAT>
F:50,98,183,187/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 51.0%; Score 74; DB 2; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0014;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSAPEYISGQINEIXYT 28
DB 25 KHSPLDPLDYGALEPHINAIQMLHHS 52

RESULT 12

T08181
superoxide dismutase (EC 1.15.1.1) (Mn) - radish
C:Species: Raphanus sativus (radish)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Apr-2000
C:Accession: T08181
R:Kwon, S.I.; An, C.S.
A:Reference number: Z16401
A:Accession: T08181
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-231 <KWO>
A:Cross-references: EMBL:AF061333; NID:G3108344; PID:G3108345
C:Genetics:
A:Gene: sod
C:Function:

Query Match 49.7%; Score 72; DB 2; Length 228;
Best Local Similarity 46.2%; Pred. No. 0.0028;
Matches 12; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSAPEYISGQINEIXY 27
DB 31 FTLPLDYGALEPAISGEIMQIHH 56

RESULT 13

E90174
superoxide dismutase [Fe] (sod) [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C:Accession: E90174
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.; arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: E90174
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-211 <KUR>
A:Cross-references: GB:AB006641; NID:GI3813460; PIDN:AAK40652.1; GSPDB:GN00155
C:Genetics:
A:Gene: sod
C:Superfamily: superoxide dismutase (Mn)

Query Match 50.3%; Score 73; DB 2; Length 211;
Best Local Similarity 51.9%; Pred. No. 0.0018;
Matches 14; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSAPEYISGQINEIXY 27
DB 9 KYELPPLPYKIDALEPYISKDIDVHY 35

RESULT 14

T08045
superoxide dismutase (EC 1.15.1.1) (Mn) precursor - pepper
C:Species: Capsicum annuum (pepper)
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 20-Apr-2000
C:Accession: T08045
R:Li, K.S.; Sun, A.C.
A:Reference number: Z16312
A:Accession: T08045
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-228 <ILK>
A:Cross-references: EMBL:AF036936; NID:g2687664; PIDN:AA88870.1; PID:g2687665
C:Genetics:
A:Gene: SOD
C:Function:

Query Match 49.7%; Score 72; DB 2; Length 228;
Best Local Similarity 46.2%; Pred. No. 0.0028;
Matches 12; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSAPEYISGQINEIXY 27
DB 31 FTLPLDYGALEPAISGEIMQIHH 56

Qy 2 YSLPELDYFSATPEYISGQINEIXY 27
::|||:||:|||||:::
Db 31 FTLPDLDPDYGALEPAISGEIMQIH 56

RESULT 22
DSPMN
superoxide dismutase (EC 1.15.1.1) (Mn) precursor - garden pea
C:Species: Pisum sativum (garden pea)
C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 11-Jun-1999
C:Accession: S18343; S15560
R:Wong-Vega, L.; Burke, J.J.; Allen, R.D.
Plant Mol Biol. 17, 1271-1274, 1991
A>Title: Isolation and sequence analysis of a cDNA that encodes pea manganese superoxide
A:Reference number: S18343; MUID:92032795; PMID:1932701
A:Molecule type: mRNA
A:A:Residues: 1-240 <WON>
A:C:Cross-references: EMBL:X60170; NID:g20901; PIDN:CAA42737.1; PID:g20902
C:Function:
A>Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
F:1-36/Domain: transit peptide (mitochondrion) #status predicted <NP>
F:37-240/Product: superoxide dismutase (Mn) #status predicted <MA>
F:64,112,201,205/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 48.3%; Score 70; DB 1; Length 240;
Best Local Similarity 46.2%; Pred. No. 0.006;
Matches 12; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 2 YSLPELDYFSATPEYISGQINEIXY 27
::|||:||:|||||:::
Db 40 FTLPDLDPDYGALEPAISGEIMQIH 56

RESULT 23
C69709
superoxide dismutase (EC 1.15.1.1) (Fe/Mn) sodF - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: C69709
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berlec,
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chai,
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrazi, E.;
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallie,
Iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapides, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauec,
Y. M.; Ogawa, K.; Ogtwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Serio,
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpatra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yanane, K.; Yasumoto, K.; Yata, K.; Yoshida,
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: C69709
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-281 <KUN>
A:C:Cross-references: GB:Z99114; GB:AL009126; NID:g2634230; PIDN:CABL3925.1; PID:g2634326
A:Experimental source: strain 168
C:Genetics:
A:Gene: sodF
C:Function:
A>Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: iron; manganese; metalloprotein; oxidoreductase
F:104,152,236,240/Binding site: iron/manganese (His, His, Asp, His) #status predicted


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RESULT 28
T42080
superoxide dismutase (EC 1.15.1.1) (Fe-Zn) sodF [validated] - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Oct-2000
C:Accession: T42080; S74129
R:Kim, E.J.; Chung, H.J.; Suh, B.; Hah, Y.C.; Roe, J.H.
J. Bacteriol. 180, 2014-2020, 1998
A:Title: Expression and regulation of the sodF gene encoding iron- and zinc-containing S
A:Reference number: Z22061; MUID:98215165; PMID:9555880
A:Accession: T42080
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-213 <KIM>
A:Cross-references: EMBL:AF012087; NID:g2707212; PIDN:AAC46274.1; PID:g2707213
R:Kim, E.J.; Kim, H.P.; Hah, Y.C.; Roe, J.H.
Eur. J. Biochem. 241, 178-185, 1996
A:Title: Differential expression of superoxide dismutases containing Ni and Fe/Zn in Str
A:Reference number: S74128; MUID:97054607; PMID:8898904
A:Accession: S74129
A:Molecule type: protein
A:Residues: 2-16 <KI2>
A:Experimental source: ATCC 10147
C:Genetics:
A:Gene: sodF
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: iron; metalloprotein; oxidoreductase; tetramer; zinc
F:2-213/Product: superoxide dismutase (Fe-Zn) #status experimental <MAT>
F:28,76,165,169/Binding site: iron (His, His, Asp, His) #status predicted
F:28,76,165,169/Binding site: iron (His, His, Asp, His) #status predicted

Query Match 46.9%; Score 68; DB 2; Length 213;
Best Local Similarity 50.0%; Pred. No. 0.01;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 2 YSLPELDYFSAPEYVIGQINEIXY 27
:|||||:|||||:|||||:
Db 4 YTLPELDYDYSALAPVISPEITELHH 29
:|||||:|||||:|||||:

RESULT 29
T06801
probable superoxide dismutase (EC 1.15.1.1) (Mn) precursor - wheat
C:Species: Triticum aestivum (common wheat)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C:Accession: T06801
R:Wu, G.; Robertson, A.J.; Wilen, R.W.; Gusta, L.V.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z15825
A:Accession: T06801
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-231 <WUG>
A:Cross-references: EMBL:U73172; NID:gl654386; PIDN:AAB68036.1; PID:gl654387
C:Genetics:
A:Gene: SOD3.2
C:Function:
A:Description: catalyzes the dismutation of superoxide radicals
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: manganese; metalloprotein; oxidoreductase
F:55,103,192,196/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 46.9%; Score 68; DB 2; Length 231;
Best Local Similarity 42.3%; Pred. No. 0.012;
Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 2 YSLPELDYFSAPEYVIGQINEIXY 27
:|||||:|||||:|||||:
Db 31 FTLPELDYDYSALAPVISPEITELHH 56
:|||||:|||||:|||||:

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RESULT 30
C48684
superoxide dismutase (EC 1.15.1.1) (Mn) 3.4 precursor - maize
C:Species: Zea mays (maize)
C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 20-Apr-2000
C:Accession: C48684
R:Zhu, D.; Scandalios, J.G.
Proc. Natl. Acad. Sci. U.S.A. 90, 9310-9314, 1993
A:Title: Maize mitochondrial manganese superoxide dismutases are encoded by a different
A:Reference number: A48684; MUID:94022365; PMID:8415698
A:Accession: C48684
A:Molecule type: mRNA
A:Residues: 1-232 <ZHU>
A:Cross-references: GB:L19463
A:Experimental source: line W64A, embryos
A>Note: the authors translated the codon GCC for residue 48 as Val and AGG for residue 1
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
F:1-29/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F:57,105,193,197/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 46.9%; Score 68; DB 2; Length 232;
Best Local Similarity 48.0%; Pred. No. 0.012;
Matches 12; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 3 SLPELDYFSAPEYVIGQINEIXY 27
:|||||:|||||:|||||:
Db 34 ALPDLSDYDGALEPVISGEIMRLHH 58
:|||||:|||||:|||||:

RESULT 31
A48684
superoxide dismutase (EC 1.15.1.1) (Mn) 3.3 precursor - maize
C:Species: Zea mays (maize)
C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 20-Apr-2000
C:Accession: A48684
R:Zhu, D.; Scandalios, J.G.
Proc. Natl. Acad. Sci. U.S.A. 90, 9310-9314, 1993
A:Title: Maize mitochondrial manganese superoxide dismutases are encoded by a different
A:Reference number: A48684; MUID:94022365; PMID:8415698
A:Accession: A48684
A:Molecule type: mRNA
A:Residues: 1-233 <ZHU>
A:Cross-references: GB:L19462
A:Experimental source: line W64A, embryos
A>Note: the authors translated the codon ATC for residue 76 as Leu and AGG for residue 1
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
F:1-29/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F:57,105,194,198/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 46.9%; Score 68; DB 2; Length 233;
Best Local Similarity 48.0%; Pred. No. 0.012;
Matches 12; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 3 SLPELDYFSAPEYVIGQINEIXY 27
:|||||:|||||:|||||:
Db 34 ALPDLSDYDGALEPVISGEIMRLHH 58
:|||||:|||||:|||||:

RESULT 32
T50831
superoxide dismutase (EC 1.15.1.1) (Mn) [similarity] - Zantedeschia aethiopica
C:Species: Zantedeschia aethiopica
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 03-Nov-2000
C:Accession: T50831
R:Lino-Neto, T.; Tavares, R.M.; Palme, K.; Pais, M.S.S.
submitted to the EMBL Data Library, September 1998

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A;Description: Expression of superoxide dismutases during senescence and regreening of Z
A;Reference number: Z25250
A;Accession: T50831
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-240 <LIN>
A;Cross-references: EMBL:AF094832; PIDN:AAC63379.1
C;Genetics:
A;Gene: Mnsod
C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; oxidoreductase
F:64,112,201,205/Binding site: manganese (His, His, Asp, His) #status predicted
Query Match 46.9%; Score 68; DB 2; Length 240;
Best Local Similarity 46.2%; Pred. No. 0.012;
Matches 12; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
QY 2 YSLPELDYEFSAPEPYISQINEIXY 27
DB 40 FSLPDLFYDGSLEPAISGEIMRIHH 65
RESULT 33
S39871
superoxide dismutase (EC 1.15.1.1) (Mn) - Haemophilus influenzae (strain Eagan)
C;Species: Haemophilus influenzae
A;Variety: strain Eagan
C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
C;Accession: S39871
R;Kroll, J.S.; Langford, P.R.; Saah, J.R.; Loynds, B.M.
Mol. Microbiol. 10, 839-848, 1993
A;Title: Molecular and genetic characterization of superoxide dismutase in Haemophilus i
A;Reference number: S39871; MUID:95020555; PMID:7934846
A;Accession: S39871
A;Molecule type: DNA
A;Residues: 1-211 <KRO>
A;Cross-references: EMBL:X73832; NID:G435652; PIDN:CAA52054.1; PID:G435653
A;Experimental source: type b, virulent strain Eagan
C;Genetics:
A;Gene: soda
C;Function:
A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; oxidoreductase
F:27,83,170,174/Binding site: manganese (His, His, Asp, His) #status predicted
Query Match 46.2%; Score 67; DB 2; Length 211;
Best Local Similarity 44.4%; Pred. No. 0.015;
Matches 12; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
QY 2 YSLPELDYEFSAPEPYISQINEIXY 28
DB 3 YTLPELGAYNALEPHFDAQTWEIHHS 29
RESULT 34
B75415
superoxide dismutase (EC 1.15.1.1) (Mn) DR1279 [similarity] - Deinococcus radiodurans (s
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 26-May-2000
C;Accession: B75415
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioreistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: B75415
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-211 <WHI>
A;Cross-references: GB:AE000513; NID:G6459022; PIDN:AAFI0851.1; PID:G645902
A;Experimental source: strain R1

C;Genetics:

A;Gene: DR1279
A;Map position: 1

C;Superfamily: superoxide dismutase (Mn)

C;Keywords: manganese; metalloprotein; oxidoreductase

F:27,81,173,177/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match

46.2%; Score 67; DB 2; Length 211;

Best Local Similarity 44.4%; Pred. No. 0.015;

Matches 12; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSAPEPYISQINEIXY 28

DB 3 YTLPELGAYNALEPHFDAQTWEIHHT 29

RESULT 35

C64182

superoxide dismutase (EC 1.15.1.1) (Mn) - Haemophilus influenzae (strain Rd KW20)

C;Species: Haemophilus influenzae

C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-May-2000

C;Accession: C64182

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J

; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: C64182

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-215 <TIGR>

A;Cross-references: GB:U32789; GB:L42023; NID:G1574642; PIDN:AAC22745.1; PID:G1574643; T

A;Experimental source: strain Rd KW20

C;Genetics:

A;Gene: soda

C;Function:

A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen

C;Superfamily: superoxide dismutase (Mn)

C;Keywords: manganese; metalloprotein; oxidoreductase

F:27,83,170,174/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match

46.2%; Score 67; DB 2; Length 215;

Best Local Similarity 44.4%; Pred. No. 0.015;

Matches 12; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSAPEPYISQINEIXY 28

DB 3 YTLPELGAYNALEPHFDAQTWEIHHS 29

RESULT 36

T50828

superoxide dismutase (EC 1.15.1.1) (Mn) 1 [similarity] - Prunus persica

C;Species: Prunus persica

C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 03-Nov-2000

C;Accession: T50828

R;Bagnoli, F.

submitted to the EMBL Data Library, October 1999

A;Reference number: Z25247

A;Accession: T50828

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-228 <BAG>

A;Cross-references: EMBL:AJ238316; PIDN:CAB56851.1

C;Genetics:

A;Gene: sod

C;Superfamily: superoxide dismutase (Mn)

C;Keywords: manganese; metalloprotein; oxidoreductase

F:52,100,189,193/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match

46.2%; Score 67; DB 2; Length 228;


```

QY      3 SLPEDLYEFSATEPYISGQINEIXY 27
       :|||:|||:|||:|||:|||:::
Db      36 TLPDLGYDFGALEPAISGEIMRLHH 60

RESULT 39
SS3456
superoxide dismutase (EC 1.15.1.1) (Mn), 23K - maize (fragments)
C:Species: Zea mays (maize)
C>Date: 01-Aug-1995 #sequence_revision 12-Apr-1996 #text_change 07-May-1999
C:Accession: S53456
R:Peldwisch, J.; Zettl, R.; Campos, N.; Palme, K.
Biochem. J. 305, 853-857, 1995
A:title: Identification of a 23 kDa protein from maize photoaffinity-labelled w
A:Reference number: S53456; MUID:95151021; PMID:7848285
A:Accession: S53456
A:Molecule type: protein
A:Residues: 1-27;28-43 <FEL>
C:Function:
A:description: catalyzes the dismutation of 2 molecules of peroxide radical to
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: metalloprotein; oxidoreductase

Query Match          45.5%; Score 66; DB 2; Length 43;
Best Local Similarity 60.0%; Pred.No. 0.0029;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 SLPEDLYEFSATEPYISGQI 22
       :|||:|||:|||:|||:|||:
Db      5 TLPDLGYDFGALEPAISGEI 24

RESULT 40
AG0493
superoxide dismutase (EC 1.15.1.1) [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C:Accession: AG0493
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prenti
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dou
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.;
Nature 413, 523-527, 2001
A:title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AG0493
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-207 <RUR>
A:Cross-references: GB:AL590842; PIDN:CAC93515.1; PID:g15981956; GSPDB:GN00175
C:Genetics:
A:Gene: soda
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: oxidoreductase

Query Match          45.5%; Score 66; DB 2; Length 207;
Best Local Similarity 48.1%; Pred.No. 0.02;
Matches 13; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY      2 YSLPELYEFSATEPYISGQINEIXYT 28
       |||||:|||:|||:|||:|||:
Db      3 YSLPSLPYAYDALEPHFDKQTWEIHHT 29

Search completed: August 24, 2004, 23:03:46
Job time : 39 secs

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